

GenCore version 5.1.6
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protein - protein search, using sw model

on: June 10, 2004, 11:04:47 ; Search time 95 seconds
(without alignments)
585.914 Million cell updates/sec

le: US-09-934-289a-18

fect score: 1146

uence: 1 MEPPGDWGPFWSTPRTDV.....EQHQTNWPNHMCCKKAKG 197

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 1586107 seqs, 282547505 residues

al number of hits satisfying chosen parameters: 1586107

imum DB seq length: 0

imum DB seq length: 2000000000

t-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase :

A_Geneseq_29Jan04:*

1: Geneseq1980s:*

2: Geneseq1980s:*

3: Geneseq2000s:*

4: Geneseq2000s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

alt No.	Score	Query Match	Length	DB ID	Description
1	1146	100.0	197	3	AAY79205 Soluble h
2	1146	100.0	197	6	ABU60682 Human sol
3	1065	92.9	193	3	AAY79204 Soluble h
4	1065	92.9	193	6	ABU60675 Human sol
5	1060	92.5	277	3	AAY79207 Membrane-
6	1060	92.5	277	6	ABU60694 Human mem
7	1060	92.5	283	2	AAY05809 Human tum
8	1060	92.5	283	2	AAY69238 Herpesvir
9	1060	92.5	283	2	AAY06488 Human tum
10	1060	92.5	283	3	AAY94721 Human TR2
11	1060	92.5	283	3	AAY95348 Human PRO
12	1060	92.5	283	3	AAY93695 Amino aci
13	1060	92.5	283	6	ABU60682 Human tum
14	1060	92.5	283	6	ABU60681 Human mem
15	1060	92.5	283	6	ABU58631 Human can
16	1060	92.5	283	6	ABU40215 Human cob
17	1060	92.5	283	6	ADA43035 Human her
18	1057	92.2	283	6	AAY60045 Human TNF
19	1057	92.2	283	2	AAY87591 Human tum
20	1057	92.2	283	3	AAY94717 Human TR2
21	1054	92.0	283	2	AAY95031 Tumour ne
22	1053	91.9	186	3	AAY79206 Soluble h
23	1053	91.9	186	6	ABU60688 Human sol
24	1052	91.8	283	2	AAY12659 Human her
25	1052	91.8	283	2	AAY05797 Herpes vi

ABU60683 Human mat
ABU60676 Human mat
ABU60695 Human mat
ABU60689 Human mat
AAY60046 Human TNF
AAY94716 Human TR2
AAY05810 Human tum
AAY60047 Human TNF
AAY94719 Human TR2
AAY05811 Human tum
AAY95322 Pig costi
AAB66980 Stu-t2 pr
AAR7865 Rabbit fi
AAR85071 Shope fib
ABJ37103 Concatame
AAR72504 p75 Tumou
ABR40141 Human cvl
ADA20590 Fragment
AAR77421 BamIP del
AAM48061 Human TNF

ALIGNMENTS

RESULT 1

AAY79205
ID AAY79205 standard; protein; 197 AA.

XX AC AAY79205;

XX DT 19-JUN-2000 (first entry)

XX DE Soluble herpesvirus entry mediator-2 (SHVEM2).

KW SHVEM-2; soluble herpesvirus entry mediator-2; TANGO-69-receptor;
KW tumour necrosis factor receptor; human; herpes simplex virus; infection;
KW cancer; inflammation; autoimmune disorder; therapy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..38

FT Protein /note= "signal peptide"

FT /note= "mature protein, also separately claimed in Claim

FT Domain 42..75

FT Domain /note= "cysteine-rich domain"

FT Modified-site 78..119

FT /note= "cysteine-rich domain"

FT Domain 110

FT /note= "N-glycosylated"

FT Domain 121..162

FT /note= "cysteine-rich domain"

FT Modified-site 173

FT /note= "N-glycosylated"

PN WO200014230-A1.

XX PD 16-MAR-2000.

XX PF 03-SEP-1999; 99WO-US020180.

XX PR 03-SEP-1998; 98US-00146950.

XX 29-JUN-1999; 99US-00342767.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX Busfield SJ;

XX WPI; 2000-256981/22.

XX N-PSDB; AAZ94195.

New nucleic acid molecule encoding herpes virus entry mediator (HVEM), either in the soluble or membrane bound form, is useful in screening assays and detection assays.

Claim 8; Fig 3; 149pp; English.

This polypeptide, the mature portion of which is also claimed, is human soluble herpesvirus entry mediator-2 (SHVEM2), a novel soluble form of membrane-bound herpesvirus entry mediator (mHVEM). The amino acid sequence was deduced from an isolated cDNA clone (see AAZ94196). SHVEM2 is a TANGO-69-receptor and member of the tumour necrosis factor receptor (TNFR) superfamily. It is thought to play a role analogous to other soluble members of the TNFR superfamily by interfering with the ability of LIGHT-TANGO-69 and lymphotoxin to bind mHVEM, and to play a role in herpes simplex virus (HSV) entry. The invention is based on the discovery of 3 cDNA molecules (see AAZ94195-97) which encode soluble forms (see AAY79204-06), and 1 cDNA molecule (see AAZ94198) that encodes a 2nd membrane-bound form (see AAY79207), of mHVEM. In addition to isolated full-length proteins and polynucleotides, and invention provides TANGO-69-receptor fusion proteins, antigenic peptides and antibodies. Also provided are recombinant expression vectors, host cells and transgenic animals in which a TANGO-69-receptor gene has been introduced or disrupted. DNA encoding HVEM, HVEM proteins and HVEM antibodies can be used in screening and detection assays (e.g. chromosomal mapping, tissue typing). HVEM proteins can also be used for regulation of cell proliferation, cell differentiation, cell survival, inflammation mast cell activity, HSV infection and/or proliferation, and/or coagulation. HVEM agonists can be used to treat disorders associated with decreased HVEM activity, e.g. proliferative disorders such as carcinoma or pathogenic infection. Antagonists can be used to treat disorders associated with increased HVEM activity, e.g. autoimmune, T cell, inflammatory and allergic inflammation disorders

Sequence 197 AA;

Query Match 100.0%; Score 1146; DB 3; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.7e-83;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MEPPGDMGPPPPWRSTPTDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSGP 60
1 MEPPGDMGPPPPWRSTPTDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSGP 60
61 YRVKEACGELTGTVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTRTEAVCG 120
61 YRVKEACGELTGTVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTRTEAVCG 120
121 CSPGHFCIVQDGDHCAACRAYATSSPGQVQKGTESQDTLCQCPPTGTFSPNGTLEECQ 180
121 CSPGHFCIVQDGDHCAACRAYATSSPGQVQKGTESQDTLCQCPPTGTFSPNGTLEECQ 180
181 HQTWNPNHMCCKKAKG 197
181 HQTWNPNHMCCKKAKG 197

3ULT 2
160682

ABU60682 standard; protein; 197 AA.

ABU60682;

06-MAY-2003 (first entry)

Human soluble Herpesvirus Entry Mediator-2 (SHVEM-2).

Human; receptor; TANGO-69 receptor; herpesvirus entry mediator; HVEM; SHVEM1; SHVEM2; SHVEM3; mHVEM2; tumour necrosis factor receptor; TNFR; immune disorder; autoimmune disorder; arthritis; graft rejection; T-cell disorder; AIDS; inflammatory disorder; bacterial infection; psoriasis; septicemia; cerebral malaria; inflammatory bowel disease; rheumatoid arthritis; osteoarthritis; allergic inflammatory disorder;

asthma; psoriasis; apoptotic disorder; rheumatoid arthritis;
systemic lupus erythematosus; insulin-dependent diabetes mellitus;
cytotoxic disorder; septic shock; cachexia; proliferative disorder;
B-cell cancer.

Homo sapiens.

US2002132297-A1.

19-SEP-2002.

21-AUG-2001; 2001US-00934289.

03-SEP-1998; 98US-00146950.

(MILL-) MILLENNIUM PHARM INC.

Busfield SU;

WPI; 2003-255106/25.

N-PSDB; ABX90365, ABX90566.

New TANGO-69 receptor polynucleotides and polypeptides, useful for treating arthritis, graft rejection, AIDS, bacterial infection, psoriasis, septicemia, cerebral malaria, inflammatory bowel disease, asthma, psoriasis, lupus.

Claim 8; Fig 3; 79pp; English.

The invention relates to an isolated nucleic acid molecule, designated as TANGO-69 receptor polynucleotide. TANGO-69 receptor refers to a portion of the proteins SHVEM1, SHVEM2, SHVEM3 and mHVEM2 (where HVEM is Herpesvirus Entry Mediator and "s" refers to a soluble form and "m" to a membrane bound form). Also included are a host cell containing TANGO-69 receptor nucleic acid, a non-human mammalian host cell containing TANGO-69 receptor nucleic acid, an isolated polypeptide that is encoded by TANGO-69 receptor nucleic acid, an antibody that selectively binds to the TANGO-69 receptor polypeptide, and identifying a compound that binds to the and/or modulates the activity of the TANGO-69 receptor polypeptide. The polynucleotides, polypeptides compounds and methods are useful for treating immune disorders such as autoimmune disorders (e.g. arthritis, graft rejection), T-cell disorders (AIDS), inflammatory disorders (e.g. bacterial infection, psoriasis, septicemia, cerebral malaria, inflammatory bowel disease, rheumatoid arthritis, osteoarthritis), allergic inflammatory disorders (e.g. asthma, psoriasis), apoptotic disorders (e.g. rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock, cachexia, and proliferative disorders (e.g. B-cell cancers). TANGO-69 receptor is a member of the TNF (tumour necrosis factor) superfamily of proteins. The present sequence represents a TANGO-69 receptor protein

Sequence 197 AA;

Query Match 100.0%; Score 1146; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.7e-83;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPPPWRSTPTDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSGP 60
Db 1 MEPPGDMGPPPPWRSTPTDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSGP 60
QY 61 YRVKEACGELTGTVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTRTEAVCG 120
Db 61 YRVKEACGELTGTVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTRTEAVCG 120
QY 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVQKGTESQDTLCQCPPTGTFSPNGTLEECQ 180
Db 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVQKGTESQDTLCQCPPTGTFSPNGTLEECQ 180
QY 181 HQTWNPNHMCCKKAKG 197
Db 181 HQTWNPNHMCCKKAKG 197

ULT 3
79204
AA79204 standard; protein; 193 AA.
AA79204;
19-JUN-2000 (first entry)
Soluble herpesvirus entry mediator-1 (SHVEM1).
SHVEM-1; soluble herpesvirus entry mediator-1; TANGO-69-receptor;
tumour necrosis factor receptor; human; herpes simplex virus; infection;
cancer; inflammation; autoimmune disorder; therapy; diagnosis.

Homo sapiens.
Key Location/Qualifiers
Peptide 1..36
Protein /note= "signal peptide"
8 /note= "mature protein, also separately claimed in Claim
Domain 42..75
Domain /note= "cysteine-rich domain"
78..119
Modified-site /note= "cysteine-rich domain"
110
Domain /note= "N-glycosylated"
121..162
Modified-site /note= "cysteine-rich domain"
173
/note= "N-glycosylated"

WO200014230-A1.
16-MAR-2000.
03-SEP-1999; 99WO-US020180.
03-SEP-1999; 98US-00146950.
29-JUN-1999; 99US-00342767.
(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Busfield SJ;
WPI; 2000-256981/22.
N-PSDB; AAZ94195.
New nucleic acid molecule encoding herpes virus entry mediator (HVEM),
either in the soluble or membrane bound form, is useful in screening
assays and detection assays.

Claim 8; Fig 1; 149pp; English.
This polypeptide, the mature portion of which is also claimed, is human
soluble herpesvirus entry mediator-1 (SHVEM1), a novel soluble form of
membrane-bound herpesvirus entry mediator (mHVEM). The amino acid
sequence was deduced from an isolated cDNA clone (see AAZ94195). SHVEM1
is a TANGO-69-receptor and member of the tumour necrosis factor receptor
(TNFR) superfamily. It is thought to play a role analogous to other
soluble members of the TNFR superfamily by interfering with the ability
of LIGHT-TANGO-69 and lymphotoxin to bind mHVEM, and to play a role in
herpes simplex virus (HSV) entry. The invention is based on the discovery
of 3 cDNA molecules (see AAZ94195-97) which encode soluble forms (see
AAZ9204-06), and 1 cDNA molecule (see AAZ94198) that encodes a 2nd
membrane-bound form (see AA79207), of mHVEM. In addition to isolated
full-length proteins and polynucleotides, and invention provides TANGO-69
-receptor fusion proteins, antigenic peptides and antibodies. Also
provided are recombinant expression vectors, host cells and transgenic
animals in which a TANGO-69-receptor gene has been introduced or
disrupted. DNA encoding HVEM, HVEM proteins and HVEM antibodies can be

used in screening and detection assays (e.g. chromosomal mapping, tissue
typing). HVEM proteins can also be used for regulation of cell
proliferation, cell differentiation, cell survival, inflammation mast
cell activity, HSV infection and/or proliferation, and/or coagulation.
HVEM agonists can be used to treat disorders associated with decreased
HVEM activity, e.g. proliferative disorders such as carcinoma or
pathogenic infection. Antagonists can be used to treat disorders
associated with increased HVEM activity, e.g. autoimmune, T cell,
inflammatory and allergic inflammation disorders

Sequence 193 AA;
Query Match 92.9%; Score 1065; DB 3; Length 193;
Best Local Similarity 100.0%; Pred. No. 4.7e-77;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPPGDWGPPTPRTRDVLRLVLTFLGAPCAPALPSCKEDEYPVGSCECPKCSFG 60
DB 1 MEPPGDWGPPTPRTRDVLRLVLTFLGAPCAPALPSCKEDEYPVGSCECPKCSFG 60
QY 61 YRVEAGGELTGVCPPTGTYIAHLNGLSKLOCOMCDPAMGLRASNCRSTENAVCG 120
DB 61 YRVEAGGELTGVCPPTGTYIAHLNGLSKLOCOMCDPAMGLRASNCRSTENAVCG 120
QY 121 CSPGHFCIVQGDHCAACRAYATSPGQVQXGTTESQDTLQNCPPPTFSPNGTLEECQ 180
DB 121 CSPGHFCIVQGDHCAACRAYATSPGQVQXGTTESQDTLQNCPPPTFSPNGTLEECQ 180
QY 181 HQTN 184
DB 181 HQTN 184

RESULT 4
ABU60675
ID ABU60675 standard; protein; 193 AA.
XX
AC ABU60675;
XX
DT 06-MAY-2003 (first entry)
XX
DE Human soluble Herpesvirus Entry Mediator-1 (SHVEM-1).
XX
KW Human; receptor; TANGO-69 receptor; herpesvirus entry mediator; HVEM;
KW SHVEM1; SHVEM2; SHVEM3; mHVEM2; tumour necrosis factor receptor; TNFR;
KW immune disorder; autoimmune disorder; arthritis; graft rejection;
KW T-cell disorder; AIDS; inflammatory disorder; bacterial infection;
KW psoriasis; septicemia; cerebral malaria; inflammatory bowel disease;
KW rheumatoid arthritis; osteoarthritis; allergic inflammatory disorder;
KW asthma; psoriasis; apoptotic disorder; rheumatoid arthritis;
KW systemic lupus erythematosus; insulin-dependent diabetes mellitus;
KW cytotoxic disorder; septic shock; cachexia; proliferative disorder;
KW B-cell cancer.
XX
OS Homo sapiens.
XX
PN US2002132297-A1.
XX
FD 19-SEP-2002.
XX
PF 21-AUG-2001; 2001US-00934289.
XX
PR 03-SEP-1998; 98US-00146950.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Busfield SJ;
XX
DR WPI; 2003-255106/25.
XX
XX N-PSDB; ABX90556, ABX90557.
XX
PT New TANGO-69 receptor polynucleotides and polypeptides, useful for
treating arthritis, graft rejection, AIDS, bacterial infection,

psoriasis, septicemia, cerebral malaria, inflammatory bowel disease, asthma, psoriasis, lupus.

Claim 8; Fig 1; 79pp; English.

The invention relates to an isolated nucleic acid molecule, designated as TANGO-69 receptor polynucleotide. TANGO-69 receptor refers to a portion of the proteins sHVM1, sHVM2, sHVM3 and mHVM2 (where HVM is Herpesvirus Entry Mediator and "s" refers to a soluble form and "m" to a membrane bound form). Also included are a host cell containing TANGO-69 receptor nucleic acid, a non-human mammalian host cell containing TANGO-69 receptor nucleic acid, an isolated polypeptide that is encoded by TANGO-69 receptor nucleic acid, an antibody that selectively binds to the TANGO-69 receptor polypeptide, and identifying a compound that binds to and/or modulates the activity of the TANGO-69 receptor polypeptide. The polynucleotides, polypeptides compounds and methods are useful for treating immune disorders such as autoimmune disorders (e.g. arthritis, graft rejection), T-cell disorders (AIDS), inflammatory disorders (e.g. bacterial infection, psoriasis, septicemia, cerebral malaria, inflammatory bowel disease, rheumatoid arthritis, osteoarthritis), allergic inflammatory disorders (e.g. asthma, psoriasis), apoptotic disorders (e.g. rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock, cachexia, and proliferative disorders (e.g. B-cell cancers). TANGO-69 receptor is a member of the TNF (tumour necrosis factor) superfamily of proteins. The present sequence represents a TANGO-69 receptor protein

Sequence 193 AA;

Query Match 92.9%; Score 1065; DB 6; Length 193;
Best Local Similarity 100.0%; Pred. No. 4.7e-77;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MEPPGDWGPFPWSTRTDVLRLVLTFLGAPCVAPALPSCKEDEYPVGSCECPKCSFG 60
1 MEPPGDWGPFPWSTRTDVLRLVLTFLGAPCVAPALPSCKEDEYPVGSCECPKCSFG 60
61 YRVKEAGELTGTVCCEPPGTYIAHNLGSLKLCQCMCDPAMGLRASNCRTENAVCG 120
61 YRVKEAGELTGTVCCEPPGTYIAHNLGSLKLCQCMCDPAMGLRASNCRTENAVCG 120
121 CSPGHFCIVQGDHCAACRAYATSSPGQVKGSTESQDTLQCNCPGTFSPNGTLESCQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQVKGSTESQDTLQCNCPGTFSPNGTLESCQ 180
181 HQTN 184
181 HQTN 184

SULT 5
Y79207

AA79207 standard; protein; 277 AA.

AA79207;

19-JUN-2000 (first entry)

Membrane-bound herpesvirus entry mediator-2 (mHVM2).

mHVM-2; membrane-bound herpesvirus entry mediator-2; TANGO-69-receptor; tumour necrosis factor receptor; human; herpes simplex virus; infection; cancer; inflammation; autoimmune disorder; therapy; diagnosis.

Homo sapiens.

Key Location/Qualifiers
Peptide 1..38
/note= "signal peptide"
Protein 39..277
/note= "mature protein, also separately claimed in Claim 8"
Domain 42..75

FT Domain /note= "cysteine-rich domain"
FT 78..119
FT /note= "cysteine-rich domain"
FT 110
FT Modified-site /note= "N-glycosylated"
FT 121..162
FT Domain /note= "cysteine-rich domain"
FT 165..186
FT Domain /note= "cysteine-rich domain (partial)"
FT Modified-site /note= "N-glycosylated"
FT 201..225
FT Domain /note= "transmembrane domain"
XX WO200014230-A1.
XX 16-MAR-2000.
XX 03-SEP-1999; 99WO-US020180.
XX 03-SEP-1998; 98US-00146950.
XX 29-JUN-1999; 99US-00342767.
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX Busfield SJ;
XX WPI; 2000-256981/22.
XX N-PSDB; AA294198.
XX New nucleic acid molecule encoding herpes virus entry mediator (HVM),
XX either in the soluble or membrane bound form, is useful in screening
XX assays and detection assays.

Claim 8; Fig 7; 149pp; English.

This polypeptide, the mature portion of which is also claimed, is human membrane-bound herpesvirus entry mediator-2 (mHVM2), a novel form of membrane-bound herpesvirus entry mediator (mHVM). The amino acid sequence was deduced from an isolated cDNA clone (see AA294198). mHVM2 is a TANGO-69-receptor and member of the tumour necrosis factor receptor (TNFR) superfamily. HVM plays a role in herpes simplex virus (HSV) entry. The invention is based on the discovery of 3 cDNA molecules (see AA294195-97) which encode soluble forms (see AAY79204-06) of mHVM, and the cDNA molecule encoding of mHVM2. In addition to isolated full-length proteins and polynucleotides, and invention provides TANGO-69-receptor fusion proteins, antigenic peptides and antibodies. Also provided are recombinant expression vectors, host cells and transgenic animals in which a TANGO-69-receptor gene has been introduced or disrupted. DNA encoding HVM, HVM proteins and HVM antibodies can be used in screening and detection assays (e.g. chromosomal mapping, tissue typing). HVM proteins can also be used for regulation of cell proliferation, cell differentiation, cell survival, inflammation mast cell activity, HSV infection and/or proliferation, and/or coagulation. HVM agonists can be used to treat disorders associated with decreased HVM activity, e.g. proliferative disorders such as carcinoma or pathogenic infection. Antagonists can be used to treat disorders associated with increased HVM activity, e.g. autoimmune, T cell, inflammatory and allergic inflammation disorders

XX Sequence 277 AA;

Query Match 92.5%; Score 1060; DB 3; Length 277;

Best Local Similarity 98.4%; Pred. No. 1.7e-76;

Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

Qy 1 MEPPGDWGPFPWSTRTDVLRLVLTFLGAPCVAPALPSCKEDEYPVGSCECPKCSFG 60
Db 1 MEPPGDWGPFPWSTRTDVLRLVLTFLGAPCVAPALPSCKEDEYPVGSCECPKCSFG 60
Qy 61 YRVKEAGELTGTVCCEPPGTYIAHNLGSLKLCQCMCDPAMGLRASNCRTENAVCG 120
Db 61 YRVKEAGELTGTVCCEPPGTYIAHNLGSLKLCQCMCDPAMGLRASNCRTENAVCG 120

121 CSPGHFCIVQDGHCAACRAYATSSPQVRQKGGTSSQDTLCQNCPPGTFSPNGTLEECQ 180
 121 CSPGHFCIVQDGHCAACRAYATSSPQVRQKGGTSSQDTLCQNCPPGTFSPNGTLEECQ 180
 181 HQT--NW 185
 181 HQTCSW 187

ULT 6

60694

ABU60694 standard; protein; 277 AA.

ABU60694;

06-MAY-2003 (first entry)

Human membrane-bound Herpesvirus Entry Mediator-2 (mHVEM-2).

Human; receptor; TANGO-69 receptor; herpesvirus entry mediator; HVEM; SHVEM1; SHVEM2; SHVEM3; mHVEM2; tumour necrosis factor receptor; TNFR; immune disorder; autoimmune disorder; arthritis; graft rejection; T-cell disorder; AIDS; inflammatory disorder; bacterial infection; psoriasis; septicaemia; cerebral malaria; inflammatory bowel disease; rheumatoid arthritis; osteoarthritis; allergic inflammatory disorder; asthma; psoriasis; apoptotic disorder; rheumatoid arthritis; systemic lupus erythematosus; insulin-dependent diabetes mellitus; cytotoxic disorder; septic shock; cachexia; proliferative disorder; B-cell cancer.

Homo sapiens.

US2002132297-A1.

19-SEP-2002.

21-AUG-2001; 2001US-00934289.

03-SEP-1998; 98US-00146950.

(MILL-) MILLENNIUM PHARM INC.

Busfield SJ;

WPI; 2003-255106/25.

N-PSDB; ABX90577, ABX90578.

New TANGO-69 receptor polynucleotides and polypeptides, useful for treating arthritis, graft rejection, AIDS, bacterial infection, psoriasis, septicaemia, cerebral malaria, inflammatory bowel disease, asthma, psoriasis, lupus.

Claim 8; Fig 7; 79pp; English.

The invention relates to an isolated nucleic acid molecule, designated as TANGO-69 receptor polynucleotide. TANGO-69 receptor refers to a portion of the proteins SHVEM1, SHVEM2, SHVEM3 and mHVEM2 (where HVEM is Herpesvirus Entry Mediator and "s" refers to a soluble form and "m" to a membrane bound form). Also included are a host cell containing TANGO-69 receptor nucleic acid, a non-human mammalian host cell containing TANGO-69 receptor nucleic acid, an isolated polypeptide that is encoded by TANGO-69 receptor nucleic acid, an antibody that selectively binds to the TANGO-69 receptor polypeptide, and identifying a compound that binds to and/or modulates the activity of the TANGO-69 receptor polypeptide. The polynucleotides, polypeptides compounds and methods are useful for treating immune disorders such as autoimmune disorders (e.g. arthritis, graft rejection), T-cell disorders (AIDS), inflammatory disorders (e.g. bacterial infection, psoriasis, septicaemia, cerebral malaria, inflammatory bowel disease, rheumatoid arthritis, osteoarthritis), allergic inflammatory disorders (e.g. asthma, psoriasis), apoptotic disorders (e.g. rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock,

CC cachexia, and proliferative disorders (e.g. B-cell cancers). TANGO-69
 CC receptor is a member of the TNF (tumour necrosis factor) superfamily of
 CC proteins. The present sequence represents a TANGO-69 receptor protein
 XX
 SQ Sequence 277 AA;

Query Match 92.5%; Score 1060; DB 6; Length 277;
 Best Local Similarity 98.4%; Pred. No. 1.7e-76;
 Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPGDWGPMPMRSTPRTDVLRLVLTFLGAPCYAPALFSCCKEDYPPVSGCCPKCSFG 60
 DB 1 MEPPGDWGPMPMRSTPRTDVLRLVLTFLGAPCYAPALFSCCKEDYPPVSGCCPKCSFG 60

QY 61 YRVKEACGELTGTVCPPPGTYIAHLNGLSKLQCMCDPAMGLRASNCSTENAVCG 120
 DB 61 YRVKEACGELTGTVCPPPGTYIAHLNGLSKLQCMCDPAMGLRASNCSTENAVCG 120

QY 121 CSPGHFCIVQDGHCAACRAYATSSPQVRQKGGTSSQDTLCQNCPPGTFSPNGTLEECQ 180
 DB 121 CSPGHFCIVQDGHCAACRAYATSSPQVRQKGGTSSQDTLCQNCPPGTFSPNGTLEECQ 180

QY 181 HQT--NW 185
 DB 181 HQTCSW 187

RESULT 7

AAW05809

ID AAW05809 standard; protein; 283 AA.

XX AC AAW05809;

XX DT 30-JUN-1997 (first entry)

XX DE Human tumour necrosis factor receptor.

XX KW Human; tumour necrosis factor; TNF; receptor; treatment; activation;
 KW inhibition; identification; agonist; antagonist; stimulation; T cell;
 KW differentiation; mediation; immune; antiviral; response; regulation;
 KW growth; protection; HIV; radiation; Chlamydia; infection;
 KW immunodeficiency; virus; autoimmune disease; inflammation; septic shock;
 KW cerebral; malaria; cachexia; B cell; cancer; graft; host; reaction;
 KW rejection; prevention; apoptosis; cytotoxicity; hybridisation probe;
 KW detection; antibody; reagent.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Peptide 1..38 /label= sig_peptide

FT Peptide 39..283 /label= mat_peptide

XX PN WO9634095-A1.

XX PD 31-OCT-1996.

XX PF 27-APR-1995; 95WO-US005058.

XX PR 27-APR-1995; 95WO-US005058.

XX (HUMA-) HUMAN GENOME SCI INC.

XX NI J, Gentz R, Rosen CA;

XX WPI; 1996-497627/49.

XX N-PSDB; AAT40048.

XX New nucleic acid encoding a human tumour necrosis factor receptor -
 PT useful for treatment of autoimmune diseases etc., in diagnosis and for
 PT drug screening.

XX

Claim 1; Page 47-48; 73pp; English.

The present sequence is the human tumour necrosis factor (TNF) receptor, which may be used for the identification of TNF receptor agonists or antagonists. TNF receptor agonists inhibit tumour growth, stimulate cell (e.g. T cell) differentiation, mediate the immune and antiviral responses, regulate growth, protect against radiation and Chlamydia infection, and can be used to treat immunodeficiencies, e.g. human immunodeficiency virus. Antagonists can be used to treat T cell mediated autoimmune disease, inflammation, septic shock, cerebral malaria, cachexia or B cell cancers, to inhibit graft-host reactions and to prevent apoptosis or cytotoxicity. Fragments of the TNF receptor encoding DNA can be used as hybridisation probes for detecting related genes. Antibodies against the protein can be used as reagents for detecting/measuring soluble forms of protein in the circulation

Sequence 283 AA;

Query Match 92.5%; Score 1060; DB 2; Length 283;
Best Local Similarity 98.4%; Pred. No. 1.8e-76;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
1 MEPPDGGPPPPWRSTPTDVLRLVLYTLFGAPCYAPALPSCKEDYYPVGSCECPKCSFG 60
1 MEPPDGGPPPPWRSTPTDVLRLVLYTLFGAPCYAPALPSCKEDYYPVGSCECPKCSFG 60
61 YRVKACGELTGTVCPCPGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
61 YRVKACGELTGTVCPCPGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
181 HQT--NW 185
181 HQTCSW 187

SUITE 8

W69238

AAW69238 standard; protein; 283 AA.

AAW69238;

21-OCT-1998 (first entry)

Herpesvirus entry mediator protein.

Entry mediator gene; herpesvirus; HVEM; tumour necrosis factor receptor;
gene expression regulator; cellular stress; inflammatory response;
lymphocyte activity regulator; autoimmune response.

Homo sapiens.

W09825967-A1.

18-JUN-1998.

05-DEC-1997; 97WO-US022278.

12-DEC-1996; 96US-0032705P.

(GETH) GENENTECH INC.

Ashkenazi AJ, Marsters SA;

WPI; 1998-348457/30.

N-PSDB; AAV44852.

Herpesvirus entry mediator polypeptide, HVEM - useful, e.g. in assays for
HVEM and to produce antibodies and transgenic animals, e.g. for drug
screening.

XX

Claim 1; Fig 1; 46pp; English.

This sequence is the herpesvirus entry mediator (HVEM) protein of the invention. The protein is useful in quantitative diagnostic assays for HVEM, in affinity purification of HVEM from recombinant cells/natural sources and in competitive-type receptor binding assays. It can also be used to generate antibodies, also useful in diagnostic assays for HVEM and affinity purification of HVEM. HVEM is believed to be a member of the tumour necrosis factor receptor (TNFR) family, and transient transfection of HVEM into human 293 cells caused marked activation of certain transacting factors, e.g. AP-1, suggesting that HVEM is involved in regulating gene expression in response to infectious stimuli and cellular stress. The predominant expression of HVEM mRNA in lymphocyte-rich tissues (e.g. spleen and peripheral blood) also suggested it may be a receptor in regulating lymphocyte activity. Antibodies produced may therefore be useful therapeutically, e.g. antagonistic antibodies may be useful to block excessive inflammatory/autoimmune response resulting from e.g. AP-1 induction, whilst agonistic antibodies may enhance HVEM regulation of such induction. The DNA may be used diagnostically, e.g. to determine if DNA and/or RNA encoding HVEM is present in cells, and to prepare HVEM polypeptide recombinantly. It is also useful to produce non-human transgenic animals (e.g. mice or rats), especially knockout animals containing cells with an altered gene encoding HVEM polypeptide. Such animals are useful in the development and screening of therapeutically useful reagents

Sequence 283 AA;

Query Match 92.5%; Score 1060; DB 2; Length 283;
Best Local Similarity 98.4%; Pred. No. 1.8e-76;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPDGGPPPPWRSTPTDVLRLVLYTLFGAPCYAPALPSCKEDYYPVGSCECPKCSFG 60

Db 1 MEPPDGGPPPPWRSTPTDVLRLVLYTLFGAPCYAPALPSCKEDYYPVGSCECPKCSFG 60

QY 61 YRVKACGELTGTVCPCPGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120

Db 61 YRVKACGELTGTVCPCPGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120

QY 121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180

Db 121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180

QY 181 HQT--NW 185

Db 181 HQTCSW 187

RESULT 9

RAY06488

ID AAY06488 standard; protein; 283 AA.

XX AAY06488;

27-SEP-1999 (first entry)

Human tumour-associated protein PRO509.

PRO1112; UNQ555; cancer; tumour necrosis factor receptor; diagnosis;
therapy; human.

Homo sapiens.

Key Location/Qualifiers

Domain 201..225

Domain /note= "transmembrane domain"

Domain 226..283

Domain /note= "cytoplasmic domain"

W09935170-A2.

15-JUL-1999.
 05-JAN-1999; 99WO-US000106.
 05-JAN-1998; 98US-0070440P.
 29-APR-1998; 98US-0083500P.
 22-MAY-1998; 98US-0086414P.
 10-JUN-1998; 98US-0088742P.
 10-NOV-1998; 98US-0107783P.
 20-NOV-1998; 98US-0109304P.
 (GETH) GENENTECH INC.
 Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA, Roy WA;
 Wood WI;
 WPI; 1999-430385/36.
 N-PSDB; AAX87265.
 Antibody against proteins expressed in neoplastic cells, useful for tumor
 diagnosis and treatment.
 Example 1; Fig 24; 162pp; English.

This sequence represents human PRO509 (UNQ329), a protein encoded by the
 novel cDNA clone DN450148 (see AAX87264), and a member of the tumor
 necrosis factor receptor family. Amplification of DN450148 was observed
 in various tumor tissues, suggesting a role in tumor formation or
 growth. Antagonists (e.g. antibodies) directed to PRO509 may have use in
 cancer therapy. The invention identifies 14 genes (see AAX87254-67) that
 are amplified in the genome of tumor cells. Such amplification is
 expected to be associated with overexpression of the gene product and to
 contribute to tumorigenesis. The encoded proteins (see AAY06477-90) may
 be useful targets for the diagnosis and/or treatment (including
 prevention) of certain cancers, and may act as predictors of the
 prognosis of tumor treatment. Antibodies that bind the proteins are
 claimed and used in claimed cancer diagnostic kits

Sequence 283 AA;

Query Match 92.5%; Score 1060; DB 2; Length 283;
 est Local Similarity 98.4%; Pred. No. 1.8e-76;
 matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
 1 MEPPDGMGPPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSFG 60
 1 MEPPDGMGPPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSFG 60
 61 YRVKEACGELGTVCBPPTTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
 61 YRVKEACGELGTVCBPPTTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
 121 CSPGHFCIVQGDHCAACRAVATSSPGORVOKGTESQDTLCONCPGTFSPNGTLEECQ 180
 121 CSPGHFCIVQGDHCAACRAVATSSPGORVOKGTESQDTLCONCPGTFSPNGTLEECQ 180
 181 HQT--NW 185
 181 HQTCSW 187

ULT 10
 94721
 AAY94721 standard; protein; 283 AA.
 AAY94721;

29-JAN-2001 (first entry)

Human TR2-receptor protein sequence.

Tumour necrosis factor-receptor related protein; TR2; human; cancer;
 chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease;

immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID;
 severely combined immunodeficiency; apoptosis inhibition;
 Alzheimer's disease; Parkinson's disease; Crohn's disease.

Homo sapiens.
 Key Location/Qualifiers
 Peptide 1..38
 Protein /note= "Signal peptide"
 39..283
 /label= TR2 receptor

WO200056405-A2.

28-SEP-2000.

22-MAR-2000; 2000WO-US007521.

22-MAR-1999; 99US-0125683P.

26-MAR-1999; 99US-0126522P.

20-MAY-1999; 99US-0135169P.

06-AUG-1999; 99US-0147383P.

(NLJJ/) NI J.

(ROSE/) ROSEN C A.

(GENT/) GENTZ R L.

Ni J, Rosen CA, Gentz RL;

WPI; 2000-594519/56.

N-PSDB; AAX28149.

Nucleic acid molecule encoding a human tumor necrosis factor receptor 2
 and its two splice variants, useful for treating arthritis or
 inflammation, cancer (such as follicular lymphomas) and immunodeficiency
 disorders.

Disclosure; Page 370; 373pp; English.

This invention relates to an isolated nucleic acid molecule encoding a
 human tumor necrosis factor (TNF)-receptor related protein TR2. Included
 in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.
 The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a
 member of the TNFR superfamily. The invention includes a method for the
 treatment of arthritis or inflammation using an antibody directed against
 a fragment of the TR2 protein. TR2 its agonists, antagonists and
 antibodies exhibit cytostatic, dermatological, antineoplastic,
 immunosuppressive, anti-allergic, antiarthritic, antiaesthetic,
 antiinflammatory, neuroprotective, neurotropic, antiparkinsonian, and
 cerebroprotective activity. The methods are useful for treating arthritis
 or inflammation, cancer (such as follicular lymphomas, carcinoma with p53
 mutations, cardiac tumors, pancreatic, breast, or prostate cancer), an
 immunodeficiency or for enhancing an in vivo leukocyte response to an
 antigen. Anti-TR2 antibodies are useful for treating, inhibiting or
 preventing autoimmune diseases (such as autoimmune haemolytic anaemia,
 dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and
 inflammatory myopathies) and immunodeficiency disorders (such as severely
 combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative
 disorder, or Nezelof syndrome-combined immunodeficiency with Igs). TR2,
 TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or
 antagonists are useful for treating or preventing autoimmune diseases and
 inhibit the growth, progression and/or metastasis of cancers. They are
 also used to activate, differentiate or proliferate cancerous cells or
 tissues, and can be used to treat diseases associated with increased cell
 survival, or the inhibition of apoptosis, e.g. Alzheimer's disease,
 Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful
 as sources for generating antibodies, as molecular weight markers. This
 sequence represents the TR2 receptor protein of the invention

Sequence 283 AA;

Query Match 92.5%; Score 1060; DB 3; Length 283;
 Best Local Similarity 98.4%; Pred. No. 1.8e-76;

Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

1 MEPPGDGPPPPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSG 60
 1 MEPPGDGPPPPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSG 60
 61 YRVKEACGELTGTVCPCPPPTTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
 61 YRVKEACGELTGTVCPCPPPTTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
 121 CSPGHFCIVQDGDHCAACRAYATSSPGORVQKGTESQDTLQCNCPGTFSPNGTLERCO 180
 121 CSPGHFCIVQDGDHCAACRAYATSSPGORVQKGTESQDTLQCNCPGTFSPNGTLERCO 180
 181 HQT--NW 185
 181 HQTCSW 187

SULT 11
 Y95348
 AAY95348 standard; protein; 283 AA.
 AAY95348;
 25-SEP-2000 (first entry)
 Human PRO509 antitumour protein.
 PRO509; human; antitumour; tumour; therapy; cytostatic; breast cancer;
 ovarian cancer; renal cancer; colorectal cancer; uterine cancer;
 prostate cancer; lung cancer; bladder cancer;
 central nervous system cancer; melanoma; leukaemia; neoplasm.
 Homo sapiens.

Key Location/Qualifiers
 Peptide 1..36
 Protein 37..283
 /label= Signal_Peptide
 /label= PRO509
 Modified-site 81..87
 /note= "N-myristoylation"
 Modified-site 89..95
 /note= "N-myristoylation"
 Modified-site 104..110
 /note= "N-myristoylation"
 Modified-site 110..114
 /note= "Asn is N-glycosylated"
 Modified-site 120..126
 /note= "N-myristoylation"
 Modified-site 153..159
 /note= "N-myristoylation"
 Modified-site 173..177
 /note= "Asn is N-glycosylated"
 Modified-site 192..201
 /note= "N-myristoylation"
 Modified-site 193..199
 /note= "N-myristoylation"
 Domain 205..221
 /note= "transmembrane domain"
 Modified-site 220..226
 /note= "N-myristoylation"
 Region 231..234
 /note= "cell attachment sequence"

WO200037638-A2.

29-JUN-2000.

02-DEC-1999; 99WO-US028565.

22-DEC-1998; 98US-0113296P.

PR 08-MAR-1999; 99WO-US005028.
 PR 21-APR-1999; 99US-0130232P.
 PR 28-APR-1999; 99US-0131445P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Marsters SA;
 PI Napier MA, Pitti RM, Wood WI;
 XX N-PSDB; AAA49727.
 DR WPI; 2000-442668/38.
 XX Novel composition to inhibit neoplastic cell growth or for treating tumor
 PT in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO219, PRO221,
 PT PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509 or PRO866.
 XX Claim 19; Fig 24; 172pp; English.

The present sequence is that of human antitumour protein PRO509, as deduced from a retinal cDNA clone (see AAA49727). PRO509 shows homology to members of the human tumour necrosis factor receptor family such as the lymphotoxin-beta receptor (11 identities) and CD40 (12 identities). A claimed method for inhibiting the growth of a tumour cell comprises exposing the tumor cell to PRO179, PRO207, PRO320, PRO219, PRO221, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509 or PRO866 (see AAY95337-49), their agonists or chimeric polypeptides incorporating them. The tumour is especially a cancer selected from breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder and central nervous system cancer, melanoma and leukaemia. Methods for the recombinant expression of the antitumour proteins are also provided

Sequence 283 AA;

Query Match 92.5%; Score 1060; DB 3; Length 283;
 Best Local Similarity 98.4%; Pred. No. 1.8e-76;
 Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPGDGPPPPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSG 60
 Db 1 MEPPGDGPPPPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSG 60
 QY 61 YRVKEACGELTGTVCPCPPPTTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
 Db 61 YRVKEACGELTGTVCPCPPPTTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
 QY 121 CSPGHFCIVQDGDHCAACRAYATSSPGORVQKGTESQDTLQCNCPGTFSPNGTLERCO 180
 Db 121 CSPGHFCIVQDGDHCAACRAYATSSPGORVQKGTESQDTLQCNCPGTFSPNGTLERCO 180
 QY 181 HQT--NW 185
 Db 181 HQTCSW 187

RESULT 12

AAY93695

ID AAY93695 standard; protein; 283 AA.

XX AAY93695;
 XX 03-OCT-2000 (first entry)

Amino acid sequence of novel polypeptide PRO509.

PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715;
 PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell; tumorigenesis;
 cancer; neoplastic cell growth; cell proliferation.

Homo sapiens.

Key Peptide Location/Qualifiers
 1..36 "signal sequence"
 81..87
 Modified-site /note= "N-myristoylation site"
 89..95
 Modified-site /note= "N-myristoylation site"
 104..110
 Modified-site /note= "N-myristoylation site"
 110..114
 Modified-site /note= "N-glycosylation site"
 120..126
 Modified-site /note= "N-myristoylation site"
 153..159
 Modified-site /note= "N-myristoylation site"
 173..177
 Modified-site /note= "N-glycosylation site"
 193..199
 Modified-site /note= "N-myristoylation site"
 195..201
 Modified-site /note= "N-myristoylation site"
 203..222
 Domain /note= "transmembrane domain"
 220..226
 Modified-site /note= "N-myristoylation site"
 231..234
 Region /note= "cell attachment sequence"

WO200037640-A2.

29-JUN-2000.

16-DEC-1999; 99WO-US030095.

22-DEC-1998; 98US-0113296P.

08-MAR-1999; 99WO-US005028.

02-JUN-1999; 99WO-US012252.

01-SEP-1999; 99WO-US020111.

15-SEP-1999; 99WO-US021090.

30-NOV-1999; 99WO-US028313.

30-NOV-1999; 99WO-US028409.

01-DEC-1999; 99WO-US028301.

02-DEC-1999; 99WO-US028565.

(GETH) GENENTECH INC.

Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;
 Wood WI;

WPI; 2000-452188/39.

N-PSDB; AAA46931.

New anti-polypeptide antibody useful in the treatment and diagnosis of
 neoplastic cell growth and proliferation.

Claim 61; Fig 24; 220pp; English.

The present sequence represents a novel human polypeptide. The
 specification describes novel polypeptides designated PRO201, PRO292,
 PRO327, PRO1265, PRO344, PRO347, PRO357, PRO715, PRO1017,
 PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in the
 genome of tumour cells. The polypeptides are believed to contribute to
 tumorigenesis. The polypeptides are useful target for the identification
 of certain cancers, and may act as predictors of the prognosis of tumour
 treatment. Antibodies against these polypeptides are useful in the
 treatment and diagnosis of neoplastic cell growth and proliferation in
 mammals

Sequence 283 AA;

very Match 92.5%; Score 1060; DB 3; Length 283;

Best Local Similarity 98.4%; Pred. No. 1.8e-76;

Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPDGMGPPWRSTPRDVLRLVLYTLFGAPCYAPALPESCKEDBYPVGSCECPKCSGP 60

Db 1 MEPPDGMGPPWRSTPRDVLRLVLYTLFGAPCYAPALPESCKEDBYPVGSCECPKCSGP 60

QY 61 YRVKEACGLTGTVCPCPPGTIAHLNGLSKLCQCMCDPAMGLASRNCSTENAVCG 120

Db 61 YRVKEACGLTGTVCPCPPGTIAHLNGLSKLCQCMCDPAMGLASRNCSTENAVCG 120

QY 121 CSPGHFCIVQGDHCAACRAYATSSPCQVKGKTESQDTLCQCPGTFSPNGTLEECQ 180

Db 121 CSPGHFCIVQGDHCAACRAYATSSPCQVKGKTESQDTLCQCPGTFSPNGTLEECQ 180

QY 181 HQT--NW 185

Db 181 HQTCSW 187

RESULT 13

AAE20852

ID AAE20852 standard; protein; 283 AA.

XX AAE20852;

AC AAE20852;

XX 01-JUL-2002 (first entry)

XX Human tumour necrosis factor receptor (TNFR) related protein.

XX Human; tumour necrosis factor receptor; TNFR-6alpha; TNFR-6beta; therapy;

KW immune system-related disorder; inflammatory disease; immunosuppressive;

KW bowel disease; encephalitis; atherosclerosis; gastrointestinal-Gen;

KW autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;

KW multiple sclerosis; Crohn's disease; autoimmune encephalitis; allergy;

KW graft versus host disease; GVHD; antiinflammatory; psoriasis; arthritis;

KW neuroprotective; antiarteriosclerotic; dermatological; aschma.

XX Homo sapiens.

OS WO200218622-A2.

XX 07-MAR-2002.

XX 24-AUG-2001; 2001WO-US026396.

XX 25-AUG-2000; 2000US-0227598P.

XX 21-NOV-2000; 2000US-0252131P.

XX 06-JUL-2001; 2001US-0303224P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Gentz RL, Ebner R, Yu G, Ruben SM, Ni J, Peng P;

XX WPI; 2002-281068/32.

XX Novel nucleic acid molecules comprising a polynucleotide encoding human

XX tumor necrosis factor receptor (TNFR)-6alpha and 6beta polypeptides

XX useful for treating disease e.g. inflammatory and autoimmune disorders.

XX Claim 36; Page 346-347; 350pp; English.

XX The invention relates to human tumour necrosis factor receptor (TNFR)-

XX 6alpha and 6beta protein and their corresponding nucleic acids. The

XX invention provides screening methods for identifying agonists and

XX antagonists of TNFR-6alpha and 6beta activity. The invention also

XX provides diagnostic and therapeutic methods for detecting and treating

XX immune system-related disorders. The method is useful for treating or

XX preventing an inflammatory disease or disorder selected from bowel

XX disease, encephalitis, atherosclerosis and psoriasis; an autoimmune

XX disease or disorder selected from systemic lupus erythematosus,

XX Crohn's disease, and

XX arthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease, and

XX autoimmune encephalitis, graft versus host disease (GVHD), and an allergy

or asthma. The present sequence is human TNFR-6alpha and TNFR-6beta related protein
Sequence 283 AA;
Query Match 92.5%; Score 1060; DB 5; Length 283;
Best Local Similarity 98.4%; Pred. No. 1.8e-76;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
1 MEPPDGMGPPPPWSTPTDVLRLVLYTLFGAPCYAPALPSCKEDYFVGSECCPKCSFG 60
1 MEPPDGMGPPPPWSTPTDVLRLVLYTLFGAPCYAPALPSCKEDYFVGSECCPKCSFG 60
61 YRVKEACGELTGTVCEPCPGTYIAHLNGLSKLQCMCDPAMGLASRNCSTENAVCG 120
61 YRVKEACGELTGTVCEPCPGTYIAHLNGLSKLQCMCDPAMGLASRNCSTENAVCG 120
121 CSPGHFCIVQDGHCAACRAVATSSPQGVKGGTSDTLQCNCPPTGTPSPNGTLEECQ 180
121 CSPGHFCIVQDGHCAACRAVATSSPQGVKGGTSDTLQCNCPPTGTPSPNGTLEECQ 180
181 HQT--NW 185
181 HQTCSW 187
RESULT 14
ABU60681
ABU60681 standard; protein; 283 AA.
ABU60681;
06-MAY-2003 (first entry)
Human membrane-bound Herpesvirus Entry Mediator (mHVEM).
Human; receptor; TANGO-69 receptor; herpesvirus entry mediator; HVEM;
SHVEM1; SHVEM2; SHVEM3; mHVEM2; tumour necrosis factor receptor; TNFR;
immune disorder; autoimmune disorder; arthritis; graft rejection;
T-cell disorder; AIDS; inflammatory disorder; bacterial infection;
psoriasis; septicemia; cerebral malaria; inflammatory bowel disease;
rheumatoid arthritis; osteoarthritis; allergic inflammatory disorder;
asthma; psoriasis; apoptotic disorder; rheumatoid arthritis;
systemic lupus erythematosus; insulin-dependent diabetes mellitus;
cytotoxic disorder; septic shock; cachexia; proliferative disorder;
B-cell cancer.
Homo sapiens.
US2002132297-A1.
19-SEP-2002.
21-AUG-2001; 2001US-00934289.
03-SEP-1998; 98US-00146950.
(MILL-) MILLENNIUM PHARM INC.
Busfield S7;
WPI; 2003-255106/25.
N-PSDB; ABX90562.
New TANGO-69 receptor polynucleotides and polypeptides, useful for
treating arthritis, graft rejection, AIDS, bacterial infection,
psoriasis, septicemia, cerebral malaria, inflammatory bowel disease,
asthma, psoriasis, lupus.
Disclosure; Fig 10; 79pp; English.
The invention relates to an isolated nucleic acid molecule, designated as
TANGO-69 receptor polynucleotide. TANGO-69 receptor refers to a portion

of the proteins SHVEM1, SHVEM2, SHVEM3 and mHVEM2 (where HVEM is
Herpesvirus Entry Mediator and "s" refers to a soluble form and "m" to a
membrane bound form). Also included are a host cell containing TANGO-69
receptor nucleic acid, a non-human mammalian host cell containing TANGO-
69 receptor nucleic acid, an isolated polypeptide that is encoded by
TANGO-69 receptor nucleic acid, an antibody that selectively binds to the
TANGO-69 receptor polypeptide, and identifying a compound that binds to the
and/or modulates the activity of the TANGO-69 receptor polypeptide. The
polynucleotides, polypeptides compounds and methods are useful for
treating immune disorders such as autoimmune disorders (e.g. arthritis,
graft rejection), T-cell disorders (AIDS), inflammatory disorders (e.g.
bacterial infection, psoriasis, septicemia, cerebral malaria,
inflammatory bowel disease, rheumatoid arthritis, osteoarthritis),
allergic inflammatory disorders (e.g. asthma, psoriasis), apoptotic
disorders (e.g. rheumatoid arthritis, systemic lupus erythematosus,
insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock,
cachexia, and proliferative disorders (e.g. B-cell cancer). TANGO-69
receptor is a member of the TNF (tumour necrosis factor) superfamily of
proteins. The present sequence represents a TANGO-69 receptor protein
Sequence 283 AA;
Query Match 92.5%; Score 1060; DB 6; Length 283;
Best Local Similarity 98.4%; Pred. No. 1.8e-76;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
QY 1 MEPPDGMGPPPPWSTPTDVLRLVLYTLFGAPCYAPALPSCKEDYFVGSECCPKCSFG 60
Db 1 MEPPDGMGPPPPWSTPTDVLRLVLYTLFGAPCYAPALPSCKEDYFVGSECCPKCSFG 60
QY 61 YRVKEACGELTGTVCEPCPGTYIAHLNGLSKLQCMCDPAMGLASRNCSTENAVCG 120
Db 61 YRVKEACGELTGTVCEPCPGTYIAHLNGLSKLQCMCDPAMGLASRNCSTENAVCG 120
QY 121 CSPGHFCIVQDGHCAACRAVATSSPQGVKGGTSDTLQCNCPPTGTPSPNGTLEECQ 180
Db 121 CSPGHFCIVQDGHCAACRAVATSSPQGVKGGTSDTLQCNCPPTGTPSPNGTLEECQ 180
QY 181 HQT--NW 185
Db 181 HQTCSW 187
RESULT 15
ABR58631
ID ABR58631 standard; protein; 283 AA.
AC ABR58631;
XX
XX 09-JUL-2003 (first entry)
XX Human cancer related protein SEQ ID NO:288.
XX Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
XX heart disease; atherosclerosis; endometriosis.
XX Homo sapiens.
XX WO2003025138-A2.
XX 27-MAR-2003.
XX 17-SEP-2002; 2002WO-US029560.
XX 17-SEP-2001; 2001US-0323469P.
XX 20-SEP-2001; 2001US-0323887P.
XX 13-NOV-2001; 2001US-0350666P.
XX 08-FEB-2002; 2002US-0355145P.
XX 08-FEB-2002; 2002US-0355257P.
XX 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX

Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
Zlotnick A;

WPI; 2003-354600/33.
N-PSDB; ACC72778.

New genes that are up-regulated or down-regulated in cancers, useful as markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.

Claim 12; Page 750; 767pp; English.

The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1031 genes up-regulated in acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer related gene nucleotide sequences which encode the proteins given in ABR58521 to ABR58709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a drug screening assay. The nucleic acid is useful as diagnostic markers or therapeutic targets. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in drug screening, particularly for identifying agents for treating these pathologies

Sequence 283 AA;

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Very Match          92.5%; Score 1060; DB 6; Length 283;
1st Local Similarity 98.4%; Pred. No. 1.8e-76;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

1  MEPPGDWGPFPWRSTPRDVLRLVLYLTLGAPCYAPALPCKEDYYPVGSCECPKCSFG 60
|||||
1  MEPPGDWGPFPWRSTPRDVLRLVLYLTLGAPCYAPALPCKEDYYPVGSCECPKCSFG 60

61  YRVKEACGEITGTVCEPCPGTGTIAHNLGSLKLCQCMCDPAMGLRASNCRSTENAVCG 120
|||||
61  YRVKEACGEITGTVCEPCPGTGTIAHNLGSLKLCQCMCDPAMGLRASNCRSTENAVCG 120

121  CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180
|||||
121  CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180

181  HQT--NW 185
|||
181  HQTCSW 187
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ch completed: June 10, 2004, 12:31:36
time : 97 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen, Ltd.

protein - protein search, using sw model

on: June 10, 2004, 12:31:43 ; Search time 46 seconds
(without alignments)
221.094 Million cell updates/sec

le: US-09-934-289A-18

fect score: 1146
uence: 1 MEPPDGMGPPWRSTPRTDV.....ECQHQTWPNHMCCKKXAG 197

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 389414 seqs, 51625971 residues

al number of hits satisfying chosen parameters: 389414

imum DB seq length: 0

imum DB seq length: 2000000000

it-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/ECTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query	Length	DB	ID	Description
1	1146	100.0	197	3	US-09-146-950-18	Sequence 19, Appl
2	1065	92.9	193	3	US-09-146-950-2	Sequence 2, Appl
3	1060	92.5	283	3	US-08-503-024-2	Sequence 2, Appl
4	1060	92.5	283	4	US-09-333-279-2	Sequence 2, Appl
5	1060	92.5	283	4	US-09-631-780-2	Sequence 2, Appl
6	1060	92.5	419	3	US-08-503-024-7	Sequence 7, Appl
7	1060	92.5	419	4	US-09-333-279-7	Sequence 7, Appl
8	1060	92.5	419	4	US-09-631-780-7	Sequence 7, Appl
9	1054	92.0	283	4	US-09-072-993C-2	Sequence 2, Appl
10	1052	91.8	283	5	PCT-US96-12374-2	Sequence 2, Appl
11	925	80.7	159	3	US-09-146-950-20	Sequence 20, Appl
12	844	73.6	155	3	US-09-146-950-4	Sequence 4, Appl
13	802.5	70.0	161	4	US-09-523-323-56	Sequence 56, Appl
14	451	39.4	77	3	US-09-146-950-25	Sequence 25, Appl
15	261	22.8	207	3	US-08-974-022-47	Sequence 47, Appl
16	261	22.8	207	3	US-08-795-445A-47	Sequence 47, Appl
17	261	22.8	207	3	US-08-795-447A-47	Sequence 47, Appl
18	261	22.8	207	3	US-08-974-186-47	Sequence 47, Appl
19	261	22.8	207	3	US-08-795-446B-47	Sequence 47, Appl
20	261	22.8	207	4	US-08-706-945D-133	Sequence 133, App
21	261	22.8	207	4	US-08-577-788C-47	Sequence 47, Appl
22	261	22.8	325	1	US-08-292-549-2	Sequence 2, Appl
23	261	22.8	325	3	US-09-043-785A-9	Sequence 9, Appl
24	261	22.8	325	5	PCT-US91-02207-2	Sequence 2, Appl
25	259	22.6	45	3	US-09-146-950-9	Sequence 9, Appl
26	259	22.6	227	3	US-08-574-022-48	Sequence 48, Appl
27	259	22.6	227	3	US-08-795-445A-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1

US-09-146-950-18
; Sequence 18, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-146-950-18

Query Match 100.0%; Score 1146; DB 3; Length 197;
Best Local Similarity 100.0%; Pred. No. 9.6e-96;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEPPDGMGPPWRSTPRTDVLRVLVLTFLGAPCYAPALPSCKEDEVPGSECCPKCSPG	60
DB	1	MEPPDGMGPPWRSTPRTDVLRVLVLTFLGAPCYAPALPSCKEDEVPGSECCPKCSPG	60
QY	61	YRVKEACGELTGTVCEPCPPGTYYTAHLNGLSKLCQCOMCDPAMGLRASRNCSTRTEAVCG	120
DB	61	YRVKEACGELTGTVCEPCPPGTYYTAHLNGLSKLCQCOMCDPAMGLRASRNCSTRTEAVCG	120
QY	121	CSPGHFCIVQGDHCAACRAVATSSPGQVKGSTESQDTLCQCPPTSPNGTLEECQ	180
DB	121	CSPGHFCIVQGDHCAACRAVATSSPGQVKGSTESQDTLCQCPPTSPNGTLEECQ	180
QY	181	HQTWPNHMCCKKXAG	197
DB	181	HQTWPNHMCCKKXAG	197

RESULT 2

US-09-146-950-2
; Sequence 2, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A


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CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
-09-146-950-2

Query Match      92.5%; Score 1065; DB 3; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.8e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MEPPGDWGPWPWRSTPTDVLRLVLYTLFLGAPCYAPALPSCKEDYFVGSCECCPKCSPG 60
1 MEPPGDWGPWPWRSTPTDVLRLVLYTLFLGAPCYAPALPSCKEDYFVGSCECCPKCSPG 60
61 YRVKEACGELTGTVCCEPCPPGTGTYIAHLNGLSKLQCMCDPAMGLRASNCSTENAVCG 120
61 YRVKEACGELTGTVCCEPCPPGTGTYIAHLNGLSKLQCMCDPAMGLRASNCSTENAVCG 120
121 CSPGHFCIVQGDHCAACRAYATSSPGQVOKGTTESQDTLQNCPPGTFSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQVOKGTTESQDTLQNCPPGTFSPNGTLEECQ 180
181 HQTN 184
181 HQTN 184

SULT 3
-08-509-024-2
Sequence 2, Application US/08509024B
Patent No. 6291207
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/08/509,024B
CURRENT FILING DATE: 1995-07-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 2
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
-08-509-024-2

Query Match      92.5%; Score 1060; DB 3; Length 283;
Best Local Similarity 98.4%; Pred. No. 7.8e-88;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

1 MEPPGDWGPWPWRSTPTDVLRLVLYTLFLGAPCYAPALPSCKEDYFVGSCECCPKCSPG 60
1 MEPPGDWGPWPWRSTPTDVLRLVLYTLFLGAPCYAPALPSCKEDYFVGSCECCPKCSPG 60
61 YRVKEACGELTGTVCCEPCPPGTGTYIAHLNGLSKLQCMCDPAMGLRASNCSTENAVCG 120
61 YRVKEACGELTGTVCCEPCPPGTGTYIAHLNGLSKLQCMCDPAMGLRASNCSTENAVCG 120
121 CSPGHFCIVQGDHCAACRAYATSSPGQVOKGTTESQDTLQNCPPGTFSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQVOKGTTESQDTLQNCPPGTFSPNGTLEECQ 180
181 HQTN 184
181 HQTN 184

SULT 4
-09-333-279-2
Sequence 2, Application US/09333279
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; Patent No. 630336
; GENERAL INFORMATION:
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: MONTGOMERY, Rebecca I.
; TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
; FILE REFERENCE: 0290-1
; CURRENT APPLICATION NUMBER: US/09/333,279
; CURRENT FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-333-279-2

Query Match      92.5%; Score 1060; DB 4; Length 283;
Best Local Similarity 98.4%; Pred. No. 7.8e-88;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPGDWGPWPWRSTPTDVLRLVLYTLFLGAPCYAPALPSCKEDYFVGSCECCPKCSPG 60
DB 1 MEPPGDWGPWPWRSTPTDVLRLVLYTLFLGAPCYAPALPSCKEDYFVGSCECCPKCSPG 60
QY 61 YRVKEACGELTGTVCCEPCPPGTGTYIAHLNGLSKLQCMCDPAMGLRASNCSTENAVCG 120
DB 61 YRVKEACGELTGTVCCEPCPPGTGTYIAHLNGLSKLQCMCDPAMGLRASNCSTENAVCG 120
QY 121 CSPGHFCIVQGDHCAACRAYATSSPGQVOKGTTESQDTLQNCPPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVQGDHCAACRAYATSSPGQVOKGTTESQDTLQNCPPGTFSPNGTLEECQ 180
QY 181 HQT--NW 185
DB 181 HQTCSW 187

RESULT 5
US-09-631-780-2
Sequence 2, Application US/09631780
Patent No. 6573058
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/631,780
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US/08/509,024B
PRIOR FILING DATE: 1995-07-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 2
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-09-631-780-2

Query Match      92.5%; Score 1060; DB 4; Length 283;
Best Local Similarity 98.4%; Pred. No. 7.8e-88;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPGDWGPWPWRSTPTDVLRLVLYTLFLGAPCYAPALPSCKEDYFVGSCECCPKCSPG 60
DB 1 MEPPGDWGPWPWRSTPTDVLRLVLYTLFLGAPCYAPALPSCKEDYFVGSCECCPKCSPG 60
QY 61 YRVKEACGELTGTVCCEPCPPGTGTYIAHLNGLSKLQCMCDPAMGLRASNCSTENAVCG 120
DB 61 YRVKEACGELTGTVCCEPCPPGTGTYIAHLNGLSKLQCMCDPAMGLRASNCSTENAVCG 120
QY 121 CSPGHFCIVQGDHCAACRAYATSSPGQVOKGTTESQDTLQNCPPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVQGDHCAACRAYATSSPGQVOKGTTESQDTLQNCPPGTFSPNGTLEECQ 180
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181 HOT--NW 188
181 HQTCSW 187

ULT 6

08-509-024-7
sequence 7, Application US/08509024B
Patent No. 6291207

GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/08/509,024B
CURRENT FILING DATE: 1995-07-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent In Ver. 2.0

EQ ID NO 7
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
08-509-024-7

Query Match 92.5%; Score 1060; DB 3; Length 419;
Best Local Similarity 97.9%; Pred. No. 1.2e-87;
Matches 184; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 MEPPGDGPPPPWSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDYFVGSCECCPKCSG 60
1 MEPPGDGPPPPWSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDYFVGSCECCPKCSG 60
61 YRVKEACGELTGTVCEPCPPGTGTYIAHLNGLSKLCQCMCDPAMGLRASNCSTENAVCG 120
61 YRVKEACGELTGTVCEPCPPGTGTYIAHLNGLSKLCQCMCDPAMGLRASNCSTENAVCG 120
121 CSPGHFCIVQDGDHCAACRAYATSSPGQVQKGTESQDTLCONCPPTGTFSPNGTLEECQ 180
121 CSPGHFCIVQDGDHCAACRAYATSSPGQVQKGTESQDTLCONCPPTGTFSPNGTLEECQ 180

181 HQTWPNH 188
181 HQTCKRIH 188

ULT 7

09-333-279-7
sequence 7, Application US/09333279
Patent No. 6303336

GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/333,279
CURRENT FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent In Ver. 2.0

EQ ID NO 7
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
09-333-279-7

Query Match 92.5%; Score 1060; DB 4; Length 419;
Best Local Similarity 97.9%; Pred. No. 1.2e-87;
Matches 184; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 MEPPGDGPPPPWSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDYFVGSCECCPKCSG 60
1 MEPPGDGPPPPWSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDYFVGSCECCPKCSG 60

QY 61 YRVKEACGELTGTVCEPCPPGTGTYIAHLNGLSKLCQCMCDPAMGLRASNCSTENAVCG 120
DB 61 YRVKEACGELTGTVCEPCPPGTGTYIAHLNGLSKLCQCMCDPAMGLRASNCSTENAVCG 120
QY 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVQKGTESQDTLCONCPPTGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVQKGTESQDTLCONCPPTGTFSPNGTLEECQ 180
QY 181 HQTWPNH 188
DB 181 HQTCKRIH 188

RESULT 8

US-09-631-780-7
Sequence 7, Application US/09631780
Patent No. 6573058
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/631,780
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US/08/509,024B
PRIOR FILING DATE: 1995-07-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 7
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-09-631-780-7

Query Match 92.5%; Score 1060; DB 4; Length 419;
Best Local Similarity 97.9%; Pred. No. 1.2e-87;
Matches 184; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEPPGDGPPPPWSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDYFVGSCECCPKCSG 60
DB 1 MEPPGDGPPPPWSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDYFVGSCECCPKCSG 60
QY 61 YRVKEACGELTGTVCEPCPPGTGTYIAHLNGLSKLCQCMCDPAMGLRASNCSTENAVCG 120
DB 61 YRVKEACGELTGTVCEPCPPGTGTYIAHLNGLSKLCQCMCDPAMGLRASNCSTENAVCG 120
QY 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVQKGTESQDTLCONCPPTGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVQKGTESQDTLCONCPPTGTFSPNGTLEECQ 180
QY 181 HQTWPNH 188
DB 181 HQTCKRIH 188

RESULT 9

US-09-072-993C-2
Sequence 2, Application US/09072993C
Patent No. 6346388
GENERAL INFORMATION:
APPLICANT: Michael R. Brigham-Burke
APPLICANT: Peter R. Young
TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
FILE REFERENCE: GH-50030
CURRENT APPLICATION NUMBER: US/09/072,993C
CURRENT FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/055,513
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 60/056,980
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/057,550
PRIOR FILING DATE: 1997-08-29

NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 283
TYPE: PRT
ORGANISM: HOMO SAPIENS
1-09-072-993C-2

Query Match 92.0%; Score 1054; DB 4; Length 283;
Best Local Similarity 97.9%; Pred. No. 2.7e-87;
Matches 183; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

1 MEPPDGMGPPPPWSTRTDVLRLVLYTLFLGAPCYAPALPCKEDYVPVSGCCPKCSG 60
1 MEPPDGMGPPPPWSTRTDVLRLVLYTLFLGAPCYAPALPCKEDYVPVSGCCPKCSG 60
61 YRVKACAGELTGTVCPCPGTYIAHLNGLSKLCQCMCDPAMGLRASNCRSTENAVCG 120
61 YRVKACAGELTGTVCPCPGTYIAHLNGLSKLCQCMCDPAMGLRASNCRSTENAVCG 120
121 CSPGHFCIVQGDHCAACRAYATSSPQGVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPQGVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
181 HQT--NW 185
181 HQTCSW 187

RESULT 10
T-US96-12374-2
Sequence 2, Application PC/TUS9612374
GENERAL INFORMATION:
APPLICANT: Northwestern University
TITLE OF INVENTION: Herpes Virus Entry Mediator
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12374
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Northrup, Thomas B.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: NOR3446P020PC
TELEPHONE: (312) 616-5400
TELEFAX: (312) 616-5460
TELEX: --

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
T-US96-12374-2

Query Match 91.8%; Score 1052; DB 5; Length 283;
Best Local Similarity 97.3%; Pred. No. 4.1e-87;
Matches 182; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

1 MEPPDGMGPPPPWSTRTDVLRLVLYTLFLGAPCYAPALPCKEDYVPVSGCCPKCSG 60

Db 1 MEPPDGMGPPPPWSTRTDVLRLVLYTLFLGAPCYAPALPCKEDYVPVSGCCPKCSG 60
QY 61 YRVKACAGELTGTVCPCPGTYIAHLNGLSKLCQCMCDPAMGLRASNCRSTENAVCG 120
Db 61 YRVKACAGELTGTVCPCPGTYIAHLNGLSKLCQCMCDPAMGLRASNCRSTENAVCG 120
QY 121 CSPGHFCIVQGDHCAACRAYATSSPQGVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
Db 121 CSPGHFCIVQGDHCAACRAYATSSPQGVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
QY 181 HQT--NW 185
Db 181 HQTCSW 187

RESULT 11
US-09-146-950-20
Sequence 20, Application US/09146950A
Patent No. 6287808
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 159
TYPE: PRT
ORGANISM: Homo sapiens
US-09-146-950-20

Query Match 80.7%; Score 925; DB 3; Length 159;
Best Local Similarity 100.0%; Pred. No. 5.7e-76;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 LPSCKEDEYVVGSECCPKCSGPGYRVKACAGELTGTVCPCPGTYIAHLNGLSKLCQCM 98
Db 1 LPSCKEDEYVVGSECCPKCSGPGYRVKACAGELTGTVCPCPGTYIAHLNGLSKLCQCM 60
QY 99 CDPAMGLRASNCRSTENAVCGSPGHFCIVQGDHCAACRAYATSSPQGVQKGTESQ 158
Db 61 CDPAMGLRASNCRSTENAVCGSPGHFCIVQGDHCAACRAYATSSPQGVQKGTESQ 120
QY 159 DTLQCNCPPTGTFSPNGTLEECQQTWPNHMCCKKAG 197
Db 121 DTLQCNCPPTGTFSPNGTLEECQQTWPNHMCCKKAG 159

RESULT 12
US-09-146-950-4
Sequence 4, Application US/09146950A
Patent No. 6287808
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 155
TYPE: PRT
ORGANISM: Homo sapiens
US-09-146-950-4

Query Match 73.6%; Score 844; DB 3; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-68;

atches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
39 LPSCKDEYVGSCECCPKSPGYRVKACGELTGTVCBPFGTYIAHLNGLSKLQCMQ 98
1 LPSCKDEYVGSCECCPKSPGYRVKACGELTGTVCBPFGTYIAHLNGLSKLQCMQ 60
99 CDPAMGLRASRNCSTENAVCCSPGHFCIVQDGHCAACRAYATSSPGORVQKGTESQ 158
61 CDPAMGLRASRNCSTENAVCCSPGHFCIVQDGHCAACRAYATSSPGORVQKGTESQ 120
159 DTLQCNCPGTFSPNGTLEECQHQTN 184
121 DTLQCNCPGTFSPNGTLEECQHQTN 146

SULT 13
Sequence 56, Application US/09523323
Patent No. 6635743
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-Liang
APPLICANT: Ruben, Steven M.
APPLICANT: Ullrich, Stephen
APPLICANT: Zhai, Yifan
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
FILE REFERENCE: 1488.065000C
CURRENT APPLICATION NUMBER: US/09/523,323
CURRENT FILING DATE: 2000-03-10
EARLIER APPLICATION NUMBER: 60/168,380
EARLIER FILING DATE: 1999-12-02
EARLIER APPLICATION NUMBER: 60/148,326
EARLIER FILING DATE: 1999-08-11
EARLIER APPLICATION NUMBER: 60/142,657
EARLIER FILING DATE: 1999-07-06
EARLIER APPLICATION NUMBER: 60/137,457
EARLIER FILING DATE: 1999-06-04
EARLIER APPLICATION NUMBER: 60/124,041
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: 09/252,656
EARLIER FILING DATE: 1999-02-19
EARLIER APPLICATION NUMBER: 60/075,409
EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 09/027,287
EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 09/003,886
EARLIER FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: 08/822,953
EARLIER FILING DATE: 1997-03-21
EARLIER APPLICATION NUMBER: 60/013,923
EARLIER FILING DATE: 1996-03-22
EARLIER APPLICATION NUMBER: 60/030,157
EARLIER FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 56
LENGTH: 161
TYPE: PRT
ORGANISM: Homo sapiens
-09-523-323-56

Query Match 70.0%; Score 802.5; DB 4; Length 161;
Best Local Similarity 95.9%; Pred. No. 66-65;
Matches 141; Conservative 1; Mismatches 2; Indels 3; Gaps 2;
41 SCKDEYVGSCECCPKSPGYRVKACGELTGTVCBPFGTYIAHLNGLSKLQCMQ 100
1 SCKDEYVGSCECCPKSPGYRVKACGELTGTVCBPFGTYIAHLNGLSKLQCMQ 60
101 PAMGLRASRNCSTENAVCCSPGHFCIVQDGHCAACRAYATSSPGORVQKGTESQ 160
61 PAMGLRASRNCSTENAVCCSPGHFCIVQDGHCAACRAYATSSPGORVQKGTESQ 119

QY 161 LCONCPGTFSPNGTLEECQHQT--NW 185
DB 120 LCONCPGTFSPNGTLEECQHQTCSW 146
RESULT 14
US-09-146-950-25
Sequence 25, Application US/09146950A
Patent No. 6287808
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 25
LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapiens
US-09-146-950-25
Query Match 39.4%; Score 451; DB 3; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.1e-33;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 121 CSPGHFCIVQDGHCAACRAYATSSPGORVQKGTESQDTLQCNCPGTFSPNGTLEECQ 180
DB 1 CSPGHFCIVQDGHCAACRAYATSSPGORVQKGTESQDTLQCNCPGTFSPNGTLEECQ 60
QY 181 HQTNPENMCKKKAKG 197
DB 61 HQTNPENMCKKKAKG 77

RESULT 15
US-08-974-022-47
Sequence 47, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Behavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids

Search completed: June 10, 2004, 12:41:24
 Job time : 47 secs

GenCore version 5.1.6
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protein - protein search, using sw model

on: June 10, 2004, 12:32:33 ; Search time 1029 Seconds
(without alignments)
53.936 Million cell updates/sec

le: US-09-934-289A-18

fect score: 1146
pence: 1 MEPPDGMGPPWRSTPRDV.....ECQHTWPNHMCCKKXG 197

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 1158786 seqs, 281726120 residues

al number of hits satisfying chosen parameters: 1158786

imum DB seq length: 0

imum DB seq length: 2000000000

t-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	ID	Description
1	1146	100.0	197	9	US-09-934-289A-18
2	1055	92.9	193	9	US-09-934-289A-2
3	1055	92.9	193	15	US-10-369-300-9
4	1060	92.5	277	9	US-09-934-289A-42
5	1060	92.5	277	15	US-10-369-300-10
6	1060	92.5	283	9	US-09-924-231-2
7	1060	92.5	283	9	US-09-934-289A-13
8	1060	92.5	283	9	US-09-935-727-31
9	1060	92.5	283	15	US-10-369-300-2
10	1060	92.5	283	15	US-10-418-242-31
11	1060	92.5	419	9	US-09-924-231-7
12	1057	92.2	283	13	US-10-020-787-2
13	1054	92.0	283	13	US-10-066-209-2
14	1053	91.9	186	9	US-09-934-289A-30
15	1053	91.9	186	15	US-10-369-300-11

16	925	80.7	159	9	US-09-934-289A-20	Sequence 20, Appl
17	844	73.6	155	9	US-09-934-289A-4	Sequence 4, Appl
18	839	73.2	149	9	US-09-934-289A-44	Sequence 44, Appl
19	838	73.1	143	9	US-09-934-289A-32	Sequence 32, Appl
20	802.5	70.0	161	15	US-10-375-680-56	Sequence 56, Appl
21	540	47.1	276	15	US-10-369-300-4	Sequence 4, Appl
22	261	22.8	207	11	US-09-405-032-130	Sequence 130, App
23	261	22.8	659	14	US-10-363-427-12	Sequence 12, Appl
24	259	22.6	184	10	US-09-852-455-8	Sequence 8, Appl
25	259	22.6	225	9	US-09-840-795-10	Sequence 10, Appl
26	259	22.6	227	11	US-09-405-032-131	Sequence 131, App
27	259	22.6	235	9	US-09-907-263-4	Sequence 4, Appl
28	259	22.6	235	10	US-09-882-735-16	Sequence 16, Appl
29	259	22.6	235	12	US-10-621-783-4	Sequence 4, Appl
30	259	22.6	235	12	US-10-622-383-4	Sequence 4, Appl
31	259	22.6	235	14	US-10-243-230-4	Sequence 4, Appl
32	259	22.6	235	14	US-10-436-826-75	Sequence 75, Appl
33	259	22.6	235	14	US-10-436-826-75	Sequence 75, Appl
34	259	22.6	257	14	US-10-313-852-10	Sequence 10, Appl
35	259	22.6	257	14	US-10-314-033-10	Sequence 10, Appl
36	259	22.6	439	15	US-10-360-101-226	Sequence 226, App
37	259	22.6	450	9	US-09-768-779A-3	Sequence 3, Appl
38	259	22.6	450	14	US-10-291-480-3	Sequence 2, Appl
39	259	22.6	461	9	US-09-800-909-2	Sequence 4, Appl
40	259	22.6	461	9	US-09-826-212-4	Sequence 2, Appl
41	259	22.6	461	9	US-09-758-124-2	Sequence 2, Appl
42	259	22.6	461	9	US-09-836-056A-17	Sequence 17, Appl
43	259	22.6	461	9	US-09-894-924-17	Sequence 17, Appl
44	259	22.6	461	9	US-09-840-707A-17	Sequence 17, Appl
45	259	22.6	461	9	US-09-800-908-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-09-934-289A-18
; Sequence 18, Application US/09934289A
; Patent No. US20020132297A1
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE
; TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: MB1098-061CPLCN1(M)
; CURRENT APPLICATION NUMBER: US/09/934,289A
; CURRENT FILING DATE: 2001-08-21
; PRIOR FILING DATE: 1999-06-29
; PRIOR FILING DATE: 1999-06-29
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1).....(38)
US-09-934-289A-18

Query Match	100.0%	Score 1146;	DB 9;	Length 197;
Best Local Similarity	100.0%	Pred. No. 7.5e-89;		
Matches 197;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MEPPDGMGPPWRSTPRDVLRVLVYTLFGAPCYAPALPSCKEDEYFVGSCECPKCSPG	60	
Db	1	MEPPDGMGPPWRSTPRDVLRVLVYTLFGAPCYAPALPSCKEDEYFVGSCECPKCSPG	60	
QY	61	YRVKACAGELTGTCVCEPCPGTYTAHLNGLSKLQCMCDPAMGLRASRNCSTRTENAVCG	120	
Db	61	YRVKACAGELTGTCVCEPCPGTYTAHLNGLSKLQCMCDPAMGLRASRNCSTRTENAVCG	120	

121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTSSQDTLCQNCPPGTFSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTSSQDTLCQNCPPGTFSPNGTLEECQ 180
181 HQTNPWPMCEKKKAG 197
181 HQTNPWPMCEKKKAG 197

RESULT 2

US-09-934-289A-2
Sequence 2, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: MB1098-061C1P1C1(M)
CURRENT APPLICATION NUMBER: US/09/934,289A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: SIGNAL
LOCATION: (1)...(38)
US-09-934-289A-2

Query Match 92.9%; Score 1065; DB 9; Length 193;
Best Local Similarity 100.0%; Pred. No. 4.9e-82;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MEPPGDWGPWPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSFG 60
1 MEPPGDWGPWPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSFG 60
61 YRVKEACGELTGTVCEPCPGTGYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
61 YRVKEACGELTGTVCEPCPGTGYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTSSQDTLCQNCPPGTFSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTSSQDTLCQNCPPGTFSPNGTLEECQ 180
181 HQTNP 184
181 HQTNP 184

RESULT 3

US-10-369-300-9
Sequence 9, Application US/10369300
Publication No. US20030215442A1
GENERAL INFORMATION:
APPLICANT: Fraser, Christopher
APPLICANT: Hancock, Wayne
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF
TITLE OF INVENTION: IMMUNE
TITLE OF INVENTION: DISORDERS USING COMBINATION THERAPY
FILE REFERENCE: 7853-255
CURRENT APPLICATION NUMBER: US/10/369,300
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: 60/358,463
PRIOR FILING DATE: 2002-02-19

NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
US-10-369-300-9

Query Match 92.9%; Score 1065; DB 15; Length 193;
Best Local Similarity 100.0%; Pred. No. 4.9e-82;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MEPPGDWGPWPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSFG 60
1 MEPPGDWGPWPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSFG 60
61 YRVKEACGELTGTVCEPCPGTGYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
61 YRVKEACGELTGTVCEPCPGTGYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTSSQDTLCQNCPPGTFSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTSSQDTLCQNCPPGTFSPNGTLEECQ 180
181 HQTNP 184
181 HQTNP 184

RESULT 4

US-09-934-289A-42
Sequence 42, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: MB1098-061C1P1C1(M)
CURRENT APPLICATION NUMBER: US/09/934,289A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 42
LENGTH: 277
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: SIGNAL
LOCATION: (1)...(38)
US-09-934-289A-42

Query Match 92.5%; Score 1060; DB 9; Length 277;
Best Local Similarity 98.4%; Pred. No. 1.9e-81;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
1 MEPPGDWGPWPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSFG 60
1 MEPPGDWGPWPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVPGSECCPKCSFG 60
61 YRVKEACGELTGTVCEPCPGTGYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
61 YRVKEACGELTGTVCEPCPGTGYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTSSQDTLCQNCPPGTFSPNGTLEECQ 180
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTSSQDTLCQNCPPGTFSPNGTLEECQ 180
181 HQTNP 185

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181 HQTCSW 187

SULT 5
-10-369-300-10
Sequence 10, Application US/10369300
Publication No. US20030215442A1
GENERAL INFORMATION:
APPLICANT: Fraser, Christopher
APPLICANT: Hancock, Wayne
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF
TITLE OF INVENTION: IMMUNE
TITLE OF INVENTION: DISORDERS USING COMBINATION THERAPY
FILE REFERENCE: 7853-255
CURRENT APPLICATION NUMBER: US/10/369,300
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: 60/358,463
PRIOR FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 277
TYPE: PRT
ORGANISM: Homo sapiens
-10-369-300-10

Query Match 92.5%; Score 1060; DB 15; Length 277;
Best Local Similarity 98.4%; Pred. No. 1.9e-81;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

1 MEPPGDWGPWPWRSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYVVGSECCPKCSFG 60
1 MEPPGDWGPWPWRSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYVVGSECCPKCSFG 60
61 YRVKEACGELTGTVCPCPPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
61 YRVKEACGELTGTVCPCPPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
121 CSPGHFCIVQDGDHCAACRAYATSSPGQVKGTTESQDTLCQNCPPGTFSPNGTLEECQ 180
121 CSPGHFCIVQDGDHCAACRAYATSSPGQVKGTTESQDTLCQNCPPGTFSPNGTLEECQ 180

181 HQT--NW 185
||||:|
181 HQTCSW 187

SULT 6
-09-924-231-2
Sequence 2, Application US/09924231
Patent No. US20020102644A1
GENERAL INFORMATION:
APPLICANT: SPAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/924,231
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 09/333,279
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 2
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
-09-924-231-2

Query Match 92.5%; Score 1060; DB 9; Length 283;
Best Local Similarity 98.4%; Pred. No. 1.9e-81;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPGDWGPWPWRSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYVVGSECCPKCSFG 60
Db 1 MEPPGDWGPWPWRSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYVVGSECCPKCSFG 60
QY 61 YRVKEACGELTGTVCPCPPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
Db 61 YRVKEACGELTGTVCPCPPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVKGTTESQDTLCQNCPPGTFSPNGTLEECQ 180
Db 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVKGTTESQDTLCQNCPPGTFSPNGTLEECQ 180
QY 181 HQT--NW 185
Db 181 HQTCSW 187

RESULT 7

US-09-934-289A-13
Sequence 13, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: MBIO98-061CPlCN1(M)
CURRENT APPLICATION NUMBER: US/09/934,289A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(38)
US-09-934-289A-13

Query Match 92.5%; Score 1060; DB 9; Length 283;
Best Local Similarity 98.4%; Pred. No. 1.9e-81;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPGDWGPWPWRSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYVVGSECCPKCSFG 60
Db 1 MEPPGDWGPWPWRSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYVVGSECCPKCSFG 60
QY 61 YRVKEACGELTGTVCPCPPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
Db 61 YRVKEACGELTGTVCPCPPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVKGTTESQDTLCQNCPPGTFSPNGTLEECQ 180
Db 121 CSPGHFCIVQDGDHCAACRAYATSSPGQVKGTTESQDTLCQNCPPGTFSPNGTLEECQ 180
QY 181 HQT--NW 185
Db 181 HQTCSW 187

RESULT 8

US-09-935-727-31
Sequence 31, Application US/09935727
Patent No. US20020150583A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REFERENCE: PF454P2

CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24
PRIORITY APPLICATION NUMBER: 60/303,224
PRIORITY FILING DATE: 2001-07-06
PRIORITY APPLICATION NUMBER: 60/252,131
PRIORITY FILING DATE: 2000-11-21
PRIORITY APPLICATION NUMBER: 60/227,598
PRIORITY FILING DATE: 2000-08-25
PRIORITY APPLICATION NUMBER: 09/518,931
PRIORITY FILING DATE: 2000-03-03
PRIORITY APPLICATION NUMBER: 60/168,235
PRIORITY FILING DATE: 1999-12-01
PRIORITY APPLICATION NUMBER: 60/146,371
PRIORITY FILING DATE: 1999-08-02
PRIORITY APPLICATION NUMBER: 60/131,964
PRIORITY FILING DATE: 1999-04-30
PRIORITY APPLICATION NUMBER: 60/131,270
PRIORITY FILING DATE: 1999-04-27
PRIORITY APPLICATION NUMBER: 60/124,092
PRIORITY FILING DATE: 1999-03-12
PRIORITY APPLICATION NUMBER: 60/121,774
PRIORITY FILING DATE: 1999-03-04
PRIORITY APPLICATION NUMBER: 09/006,352
PRIORITY FILING DATE: 1998-01-13
PRIORITY APPLICATION NUMBER: 60/035,496
PRIORITY FILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 31
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
S-09-935-727-31
Query Match 92.5%; Score 1060; DB 9; Length 283;
Best Local Similarity 98.4%; Pred. No. 1.9e-81;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
Y 1 MEPPGDWGPWPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVGVGSECCPKCSPG 60
b 1 MEPPGDWGPWPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVGVGSECCPKCSPG 60
Y 61 YRVKEACGELTGTVCCEPCPGTYIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
b 61 YRVKEACGELTGTVCCEPCPGTYIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
Y 121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
b 121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
Y 181 HQT--NW 185
b 181 HQTKCSW 187
RESULT 9
US-10-369-300-2
Sequence 2, Application US/10369300
Publication No. US20030215442A1
GENERAL INFORMATION:
APPLICANT: Fraser, Christopher
APPLICANT: Hancock, Wayne
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF
TITLE OF INVENTION: IMMUNE
TITLE OF INVENTION: DISORDERS USING COMBINATION THERAPY
FILE REFERENCE: 7853-255
CURRENT APPLICATION NUMBER: US/10/369,300
CURRENT FILING DATE: 2003-02-19
PRIORITY APPLICATION NUMBER: 60/358,463
PRIORITY FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patent in version 3.1
SEQ ID NO 2

LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-10-369-300-2
Query Match 92.5%; Score 1060; DB 15; Length 283;
Best Local Similarity 98.4%; Pred. No. 1.9e-81;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
QY 1 MEPPGDWGPWPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVGVGSECCPKCSPG 60
Db 1 MEPPGDWGPWPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVGVGSECCPKCSPG 60
QY 61 YRVKEACGELTGTVCCEPCPGTYIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
Db 61 YRVKEACGELTGTVCCEPCPGTYIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
Db 121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLQCNCPPTGTFSPNGTLEECQ 180
QY 181 HQT--NW 185
Db 181 HQTKCSW 187
RESULT 10
US-10-418-242-31
Sequence 31, Application US/10418242
Publication No. US20040013664A1
GENERAL INFORMATION:
APPLICANT: Gentz et al.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REFERENCE: PF454F3
CURRENT APPLICATION NUMBER: US/10/418,242
CURRENT FILING DATE: 2003-04-18
PRIORITY APPLICATION NUMBER: 60/373,604
PRIORITY FILING DATE: 2002-04-19
PRIORITY APPLICATION NUMBER: 09/935,727
PRIORITY FILING DATE: 2001-08-24
PRIORITY APPLICATION NUMBER: 60/303,224
PRIORITY FILING DATE: 2001-07-06
PRIORITY APPLICATION NUMBER: 60/252,131
PRIORITY FILING DATE: 2000-11-21
PRIORITY APPLICATION NUMBER: 60/227,598
PRIORITY FILING DATE: 2000-08-25
PRIORITY APPLICATION NUMBER: 09/518,931
PRIORITY FILING DATE: 2000-03-03
PRIORITY APPLICATION NUMBER: 60/168,235
PRIORITY FILING DATE: 1999-12-01
PRIORITY APPLICATION NUMBER: 60/146,371
PRIORITY FILING DATE: 1999-08-02
PRIORITY APPLICATION NUMBER: 60/131,964
PRIORITY FILING DATE: 1999-04-30
PRIORITY APPLICATION NUMBER: 60/131,279
PRIORITY FILING DATE: 1999-04-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 51
SEQ ID NO 31
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-10-418-242-31
Query Match 92.5%; Score 1060; DB 15; Length 283;
Best Local Similarity 98.4%; Pred. No. 1.9e-81;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
QY 1 MEPPGDWGPWPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVGVGSECCPKCSPG 60
Db 1 MEPPGDWGPWPWRSTPRDVLRLVLYTLFLGAPCYAPALPSCKEDEVGVGSECCPKCSPG 60
QY 61 YRVKEACGELTGTVCCEPCPGTYIAHLNGLSKLQCCQCDPAMGLRASRNCSTENAVCG 120

181 HQT--NW 185
||| :||
181 HQTCSW 187

!SULT 14

-09-934-289A-30

Sequence 30, Application US/09934289A

Patent No. US20020132297A1

GENERAL INFORMATION:

APPLICANT: Busfield, Samantha J.

TITLE OF INVENTION: NOVEL MOLECULES OF THE

TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: M81098-061C1C1N1(M)

CURRENT APPLICATION NUMBER: US/09/934,289A

CURRENT FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: US 09/342,767

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: US 09/146,950

PRIOR FILING DATE: 1998-09-03

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 30

LENGTH: 186

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SIGNAL

LOCATION: (1)...(38)

-09-934-289A-30

Query Match 91.9%; Score 1053; DB 9; Length 186;
Best Local Similarity 99.5%; Pred. No. 4.8e-81;
Matches 182; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MEPPGDWGGPPWRSTPTDVLRLVLYLTLFLGAPCYAPALPSCCKEYYPVGSCECCPKCSFG 60
|||
1 MEPPGDWGGPPWRSTPTDVLRLVLYLTLFLGAPCYAPALPSCCKEYYPVGSCECCPKCSFG 60
|||
61 YRVKEACGELTGTVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
|||
61 YRVKEACGELTGTVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
|||
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180
|||
121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180
|||
181 HQT 183
|||
181 HQT 183

!SULT 15

-10-369-300-11

Sequence 11, Application US/10369300

Publication No. US20030215442A1

GENERAL INFORMATION:

APPLICANT: Fraser, Christopher

APPLICANT: Hancock, Wayne

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF

TITLE OF INVENTION: IMMUNE

TITLE OF INVENTION: DISORDERS USING COMBINATION THERAPY

FILE REFERENCE: 7853-255

CURRENT APPLICATION NUMBER: US/10/369,300

CURRENT FILING DATE: 2003-02-19

PRIOR APPLICATION NUMBER: 60/358,463

PRIOR FILING DATE: 2002-02-19

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn version 3.1

SEQ ID NO 11

LENGTH: 186

! TYPE: PRT
! ORGANISM: Homo sapiens
US-10-369-300-11

Query Match 91.9%; Score 1053; DB 15; Length 186;
Best Local Similarity 99.5%; Pred. No. 4.8e-81;
Matches 182; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPPGDWGGPPWRSTPTDVLRLVLYLTLFLGAPCYAPALPSCCKEYYPVGSCECCPKCSFG 60
Db 1 MEPPGDWGGPPWRSTPTDVLRLVLYLTLFLGAPCYAPALPSCCKEYYPVGSCECCPKCSFG 60
|||
Qy 61 YRVKEACGELTGTVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
Db 61 YRVKEACGELTGTVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
|||
Qy 121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180
Db 121 CSPGHFCIVQGDHCAACRAYATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEECQ 180
|||
Qy 181 HQT 183
Db 181 HQT 183

Search completed: June 10, 2004, 12:58:46
Job time : 1030 secs

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protein - protein search, using sw model

on: June 10, 2004, 12:08:03 ; Search time 45 Seconds
(without alignments)
421.105 Million cell updates/sec

le: US-09-934-289a-18
fect score: 1146
uence: 1 MEPPGDWGPWPRTPTDV.....ECQHQTWPNHMCCKKXG 197

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 283366 seqs, 96191526 residues

al number of hits satisfying chosen parameters: 283366

imum DB seq length: 0

imum DB seq length: 2000000000

t-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase :

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	DB ID	Description
1	261	22.8	325	2	B43692
2	259	22.6	461	1	A35356
3	256.5	22.4	305	2	A46476
4	255	22.3	348	2	T28673
5	254.5	22.2	349	2	D36858
6	254	22.2	277	2	A60771
7	254	22.2	349	2	D2175
8	239.5	20.9	435	2	I34182
9	238	20.8	326	1	GVZML
10	236.5	20.6	271	2	I2783
11	211.5	18.5	272	2	I48700
12	208	18.2	425	1	A26431
13	203	17.7	474	2	B38634
14	202	17.6	459	2	I48854
15	199	17.4	416	1	UNO006
16	198.5	17.3	327	2	A46484
17	197	17.2	324	2	J23395
18	196.5	17.1	427	1	GQHTUN
19	191.5	16.7	651	2	J27705
20	188.5	16.4	277	2	J37552
21	183.5	16.0	335	2	A40036
22	182.5	15.9	314	2	I37383
23	178.5	15.6	250	1	A49053
24	169.5	14.8	256	2	B32393
25	169.5	14.8	454	1	GQMT1
26	169	14.7	461	2	J43302
27	165.5	14.4	461	1	GQRTT1
28	160	14.0	595	2	A42086
29	154.5	13.5	255	2	I38426

30 148 12.9 1786 1 MMHUB1
31 145.5 12.7 493 2 JC5486
32 141 12.3 1274 2 T42017
33 140.5 12.3 260 1 A46517
34 140.5 12.3 455 1 GQHTU1
35 139.5 12.2 5376 2 T42215
36 134 11.7 2824 2 T22759
37 132.5 11.6 4391 2 A38096
38 131.5 11.5 1786 1 MMMSB1
39 128 11.2 1620 2 T27283
40 127 11.1 1797 2 A5677
41 126 11.0 1557 2 T28811
42 125.5 11.0 1574 2 T13954
43 125.5 11.0 3707 2 S18252
44 124.5 10.9 2524 2 A35844
45 123.5 10.8 1372 2 T25933

ALIGNMENTS

RESULT 1

B43692
T2 protein - rabbit fibroma virus
C:Species: rabbit fibroma virus, Shope fibroma virus
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Sep-2003
C:Accession: B43692
R:Upton, C.; DeLange, A.M.; McFadden, G.
Viology 160, 20-30, 1987
A>Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric
A:Reference number: A43692; MUID: 87321103; PMID:2820128
A:Accession: B43692
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <UPT>
A:Cross-references: GB:M17433
C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology
F:64-105/Domain: NGF receptor repeat homology <NG2>
F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 22.8%; Score 261; DB 2; Length 325;
Best Local Similarity 33.3%; Pred. No. 6.8e-12;
Matches 58; Conservative 23; Mismatches 81; Indels 12; Gaps 6;

QY 20 VRLVLVLTGACGYAPALP-----SCDEYFVGVSECCPKSPGYRVKEAGELTGT 73
Db 1 MRLTALVGV-VVYGVDDVYSSNQKCGHDYKDGCCASCHPGFYASRLCGPGSNT 59
QY 74 VCEPCPPGTYYIAHLNGLSKLCQCMCPAMG-LRASRNCSTENAVCGSPGHFICIVDQ 132
Db 60 VCSCEDGTFTASTNHAPACVSCR--CPCTGHLSESPCDRTHRVNCSTGYCLLKQ 117
QY 133 DHCACRAYATSPGQVRQKGTESQDTLQCNPPGTFPSN-GTLECCQHTNW 185
Db 118 NGCRIC-APQTKCPAGYGVSGHTAGDTLCEKCPPTYSLSPTERCSTSFNY 170

RESULT 2

A5356
tumor necrosis factor receptor 2 precursor [validated] - human
N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 27-Oct-2003
C:Accession: A35356; A36475; A48416; A36007; A3666; B35010; I38094
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerry, R.; Dower, S.K.
Science 248, 1019-1023, 1990
A>Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
A:Reference number: A35356; MUID: 90260639; PMID:2160731
A:Accession: A35356
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <SM>
A:Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186

Matches 56; Conservative 22; Mismatches 66; Indels 22; Gaps 6;

QY 35 YAPALPS-CKEDEV--PVGSECCPKCSFGYRVKEAGELTGVCEPFGTYIAHLNGLS 91
Db :
32 YAPEPGSTCLRREYYDQTAAQMCSCSKSPQHAKVFCTKTSDDVCDSCEDSTVTQLWNWVP 91
Db :
QY 92 KLCQQCMCPANGLASRN-----CSRTENAVCCSCHFCIVQGDGHCAACRAYATSS 145
Db :
92 ECLSC-----GSRCSQDVETQACTEONRRICTRGWYCALSKBGGRLCAPLRKR 144
Db :
QY 146 PQGRVOKGGETSQDTLQCNCPPGTFS-PNGTLRECQHQHTNWPNHMC 190
Db :
145 PGFGVARPGTSTDVVCKPCAPGTFSNTSSDICK----PHQIC 185
Db :

RESULT 3

A46476

B cell-associated surface molecule CD40, long splice form - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000

C:Accession: A46476; A46515

R:Torres, R.M.; Clark, E.A.

J. Immunol. 148, 620-626, 1992

A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine CD40 gene.

A:Reference number: A46476; MUID:92105763; PMID:1370315

A:Accession: A46476

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-305 <OR>

A:Cross-references: GB:M83312; NID:g1553058

A>Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIPI:75207)

A:Note: This translation is not annotated in Genbank entry MUSCD40A, release 113.0

R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J. Immunol. 149, 3921-3926, 1992

A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.

A:Reference number: A46515; MUID:93094586; PMID:1281194

A:Accession: A46515

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-287, 'LV' <GRI>

A:Cross-references: GB:M83312; NID:g1553058; PID:NAB08705.1; PID:g1553059; GB:M94126; N

A:Experimental source: BALE/C, liver

A>Note: sequence extracted from NCBI backbone (NCBIPI:120357)

C:Comment: For an alternative splice form, see PIR:A46515.

C:Comment: For an alternative splice form, see PIR:A46515.

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: alternative splicing; transmembrane protein

P:105-144/Domains: NGF receptor repeat homology <NGF>

Query Match 22.4%; Score 256.5; DB 2; Length 305;
Best Local Similarity 34.4%; Pred. No. 1.4e-11;
Matches 53; Conservative 20; Mismatches 72; Indels 9; Gaps 3;

QY 41 SCKDEYPVGSCCFKCSFGYRVKEAGELTGVCEPFGTYIAHLNGLSKLCQQMCD 100
Db :
25 TUSDQYLHDGQCDLDPGSLTSHCTALEKTQCHPDSDGEFSQAWREIRCHQRHCE 84
Db :
QY 101 PAWLGLASRNCSTRTENAVCGSPGFHCIVQGDGHCAACRAYATSSPGORVKGGTESOPT 160
Db :
85 PNQGLRKVEKGTAESDVTCTKEGQHCITSKD---CEACAQHTPCIPGFGVWMEMATETTD 141
Db :
QY 161 LCQNCPPTFSNGTL-BECQHTNWPNHMECK 193
Db :
142 VCHPCPVGFFNSQSILFKC-----YFWTSCEDK 170
Db :

RESULT 4

T28623

hypothetical protein G2R - variola major virus

C:Species: variola major virus

C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Sep-2003

C:Accession: T28623

R:Massung, R.F.; Eposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin,

```

QY 21 LRLVLVLTFLGAPC-----YAPALPSCKEDEVPGSECCPKSPGYRVKAEACGEL 70
DB 1 MKSVLYLXILFLSCIIINGROAAPYPNGKCKDTYKRNHLCCLSCPPGYASRLCDSK 60
QY 71 TGTVCBPQPGYIAHLNGLSKLCQC-MCDPAMGLRASRNCSTRNAVCCSGPHCIV 129
DB 61 TNYCTQPCSGGFTTRNNHLPACLSNGRCN--SNQVETRSCNTHNRICSCSPGYVCLL 118
QY 130 QGDHCHCAACRAYATSPGORVGKGTESQDTLQCNCPPGTFSFN-GTLEECQHQTN 184
DB 119 KGSSGCKACVSTKCGIGYGV-SGHTSVGDVICSPCGFGTYSHTVSSADKCEPVN 173

RESULT 6
A60771
B-cell activation protein CD40 precursor - human
N/Alternate names: B-cell surface antigen Bp50
C/Species: Homo sapiens (man)
C/Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C/Accession: S04460; A60771
R/Stamenkovik, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A/Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A/Reference number: S04460; MUID:89356608; PMID:2475341
A/Accession: S04460
A/Molecule type: mRNA
A/Residues: 1-277 <STA>
A/Cross-references: EMBL:X60592; NID:G29850; PIN:CAA43045.1; PID:G29851
R/Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A/Title: Biochemical characteristics and partial amino acid sequence of the receptor-like
A/Reference number: A60771; MUID:89093941; PMID:2463309
A/Accession: A60771
A/Molecule type: protein
A/Residues: 21-50 <BRA>
A/Experimental source: Burkitt lymphoma cell line Raji
C/Genetics:
A/Gene: GDB:CD40
A/Cross-references: GDB:215268; OMIM:109535
A/Map position: 20q12-20q13.2
C/Superfamily: CD27 antigen; NGF receptor repeat homology
C/Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F/21-193/Domain: extracellular #status predicted <EXT>
F/194-215/Domain: transmembrane #status predicted <TM>
F/216-277/Domain: intracellular #status predicted <CYT>
F/153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.2%; Score 254; DB 2; Length 277;
Best Local Similarity 31.1%; Pred. No. 1.9e-11;
Matches 56; Conservative 30; Mismatches 78; Indels 16; Gaps 5;

QY 20 VLRLVLVLTFLGAPCAPAL-----PSCKEDEVPGSECCPKSPGYRVKAEACGELTCTV 74
DB 1 MWRLPQCVLWG--CLLVAVHPPTACREKQYLINSCCLSQCPGKQLVSDCTEFTETE 58
QY 75 CBFCPPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTRNAVCCSGPHFCIVQGDH 134
DB 59 CLPCESEFLDTWNRETHCHQKHYCDPNLGLRVQKGTSETDTICTCEGWHC---TSEA 115
QY 135 CAACRAYATSPGORVGKGTESQDTLQCNCPPGTFS-PNGTLEECQHQTNPVNHMEKK 193
DB 116 CBSCVLHRSCTSPFGVKGYATYGVSDTICEPCPVGFNVSFAFEKCHPWTs-----CETK 170

RESULT 7
D72175
G2R protein - variola minor virus (strain Garcia-1966)
C/Species: variola minor virus
C/Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 15-Sep-2003
C/Accession: D72175

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Cross-references: EMBL:X87128; NID:9809043; PIDN:CAA60618.1; PID:9809044
;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homology
;Keywords: cytokine receptor; transmembrane protein
;1-22/Domain: signal sequence #status predicted <SIG>
;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
;40-77/Domain: NGF receptor repeat homology <NG1>
;79-120/Domain: NGF receptor repeat homology <NG2>
;166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 17.7%; Score 203; DB 2; Length 474;
Best Local Similarity 28.1%; Pred. No. 1.3e-07;
Matches 52; Conservative 21; Mismatches 90; Indels 22; Gaps 7;

20 VLRLVLYLTFELGAPCYAPALPSCKEDEV-PVSGE-----CCPKCSGYRVKEACGE 69
11 VPELQWATGHTVPAQVLTLYKPEPGVECOISYVDRAQMCCKAPPGQVYKFCNK 70
70 LGTVCEPCPPGTYIAHLNGLSKLQCC-QMCDPAMGLRASNCSTENAVCGSPGHFC 127
71 TSDTVCADCEASMYTVQVNNQFRTCLSCSSCTTDQVEIRA---CTKQNRVCAEAGRYC 127
128 IVQ-DGDHCAACRAVATSSPGORVQKGTESQDTLCQNCPPGNTS-PNGTLEECQHQTNW 185
128 ALKTHSGRCQRMUSKCGPGFGVASSRAPNGNVLCACAPGTFSDTTSSTVCR----- 182
186 PNHMC 190
183 PHRIC 187

RESULT 14
18854
;Species: Mus musculus (house mouse)
;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 27-Oct-2003
;Accession: I48854
;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
;Genome 5, 726-727, 1994
;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
;Reference number: I48854; MUID:95178848; PMID:7873884
;Accession: I48854
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: mRNA
;Residues: 1-459 <RES>

Cross-references: EMBL:X76401; NID:9433830; PIDN:CAA53981.1; PID:9433831
;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homology
;151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 17.6%; Score 202; DB 2; Length 459;
Best Local Similarity 30.5%; Pred. No. 1.5e-07;
Matches 43; Conservative 19; Mismatches 69; Indels 10; Gaps 5;

53 CCKPCSPGYRVKEACGELTGTVCCEPPTGTYIAHLNGLSKLQCC-QMCDPAMGLRASNC 111
39 CCAKCPGGQVYKHFNCSTDTVCADCEASMYTVQVNNQFRTCLSCSSC---STDQVETAC 96
112 SRTEAVCGSPGHFCIVQ-DGDHCAACRAVATSSPGORVQKGTESQDTLCQNCPPGTF 170
97 TKQNRVCAEAGRYCAKTHSGSCRCQRLSKCGFGVASSRAPNGNVLCACAPGTF 156
171 S-PNGTLEECQHQTNWPNHMC 190
157 SDTTSSTVCR-----PHRIC 172

RESULT 15
N0006
;Species: Gallus gallus (chicken)
;Alternate names: NGF receptor
;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
;Accession: JN0006; A60504
;Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reid

Neuron 2, 1123-1134, 1999
A>Title: Structure and developmental expression of the nerve growth factor receptor in the
A;Reference number: JN0006; MUID:90166579; PMID:2560385
A;Accession: JN0006
A;Molecule type: mRNA
A;Residues: 1-416 <LAR>
A;Experimental source: embryonic chick brain
R;Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A>Title: Structure and developmental expression of the chicken NGF receptor.
A;Reference number: A60504; MUID:90152140; PMID:2154393
A;Accession: A60504
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 21-35 'Y', 37-172 'K', 174-275 'S', 277-395 'R', 397-416 <HEU>
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells.
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of the
C;Comment: This protein is thought to form a high-affinity receptor when it associates with
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; tyrosine
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-416/Product: nerve growth factor receptor #status predicted <MAT>
F;21-239/Domain: extracellular #status predicted <EXT>
F;24-57/Domain: NGF receptor repeat homology <NG1>
F;59-100/Domain: NGF receptor repeat homology <NG2>
F;101-139/Domain: NGF receptor repeat homology <NG3>
F;141-181/Domain: NGF receptor repeat homology <NG4>
F;189-237/Region: serine/threonine-rich
F;240-261/Domain: transmembrane #status predicted <MEM>
F;262-416/Domain: intracellular #status predicted <INT>
F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.4%; Score 199; DB 1; Length 416;
Best Local Similarity 31.7%; Pred. No. 2.3e-07;
Matches 53; Conservative 26; Mismatches 66; Indels 22; Gaps 9;

QY 37 PALPS-----CKEDYFVSGECCPKCSGYRVKEACGELTGTVCCEPPTG-TYIAHLNG 89
DB 13 PAGPTWGSKEKCLTMVTTSGECCACNLGEGVYVQPG-VNQTVCPECLDSVTYSPTVSA 71
QY 90 LSKCLQCCQCDPAMGLRA-SRNCSTENAVCGSPGHFCIVQGDHCAACRAVATSSPGQ 148
DB 72 TEPCKPCTQC---VGLHSMGAFVCSDDAVCRCAVGYF---QD-ELSGSKCEKSCICEVGF 124
QY 149 RVQKGTESQDTLCQNCPPGTFSPNGT-LEECQHQTNWPNHMCCKK 194
DB 125 GLMFPCCRDSQTVCECPGTFSDANFVDPD-----LPCTICEENE 166

Search completed: June 10, 2004, 12:35:00
Job time : 47 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen, Ltd.

protein - protein search, using sw model

n on: June 10, 2004, 11:06:27 ; Search time 38 Seconds
(without alignments)
269,943 Million cell updates/sec

US-09-934-289A-18

Effect score: 1146
quence: 1 MEPPGDWGPWPWRSTPTDV.....ECQHTNPNHMCCKKAKG 197

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 141681 seqs, 52070155 residues

tal number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

tabase : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	Length	DB ID	Description
1	1057	92.2	283	1	TR14_HUMAN
2	266.5	23.3	349	1	Q8UYA7 camelox vi
3	261	22.8	325	1	VT2_SFVKA
4	259	22.6	461	1	TR1B_HUMAN
5	256.5	22.4	289	1	TNR5_MOUSE
6	254.5	22.2	349	1	CRMB_VARV
7	254	22.2	277	1	TNR5_HUMAN
8	243.5	21.2	351	1	CRMB_COWPX
9	242	21.1	269	1	TNR5_BOVIN
10	239.5	20.9	435	1	TNR3_HUMAN
11	238	20.8	326	1	VT2_MXVL
12	236.5	20.6	271	1	TNR4_RAT
13	231	20.2	300	1	TR6B_HUMAN
14	218	19.0	417	1	TR16_MOUSE
15	217	18.9	415	1	TNR3_MOUSE
16	211.5	18.5	272	1	TNR4_MOUSE
17	208	18.2	425	1	TR16_RAT
18	203	17.7	474	1	TR1B_MOUSE
19	202	17.6	332	1	TNR6_PIG
20	199	17.4	416	1	TR16_CHICK
21	198.5	17.3	327	1	TNR6_MOUSE
22	197	17.2	324	1	TNR6_RAT
23	197	17.2	401	1	T11B_HUMAN
24	196.5	17.1	427	1	TR16_HUMAN
25	196	17.1	401	1	T11B_MOUSE
26	193	16.8	401	1	T11B_RAT
27	192	16.8	655	1	TR21_HUMAN
28	190	16.6	616	1	TR11_HUMAN
29	189	16.5	655	1	TR21_MOUSE
30	188.5	16.4	277	1	TNR4_HUMAN
31	186	16.2	417	1	TR25_HUMAN
32	183.5	16.0	335	1	TNR6_HUMAN
33	183	16.0	323	1	TNR6_BOVIN

34	182.5	15.9	625	1	TR11_MOUSE
35	180	15.7	204	1	TR26_MOUSE
36	178.5	15.6	250	1	TNR7_MOUSE
37	169.5	14.8	256	1	TNR9_MOUSE
38	169.5	14.8	454	1	TR1A_MOUSE
39	169	14.7	461	1	TR1A_PIG
40	168	14.7	471	1	TR1A_BOVIN
41	165.5	14.4	461	1	TR1A_RAT
42	164	14.3	498	1	TNR8_MOUSE
43	160	14.0	595	1	TNR8_HUMAN
44	157.5	13.7	176	1	TR23_MOUSE
45	155	13.5	198	1	TR22_MOUSE

ALIGNMENTS

RESULT 1					
TR14_HUMAN					
ID	TR14_HUMAN	STANDARD;	PRT;	283	AA.
AC	Q92956; Q8WXR1; Q96J31; Q9UM65;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Tumor necrosis factor receptor superfamily member 14 precursor				
DE	(Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2)				
DE	(Tr2).				
GN	TNFRSF14 OR HVEM OR HVFA.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Cervical adenocarcinoma;				
RX	MEDLINE=37053782; PubMed=8898196;				
RA	Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;				
RT	"Herpes simplex virus-1 entry into cells mediated by a novel member of				
RT	the TNF/NGF receptor family.";				
RL	Cell 87:427-436(1996).				
[2]					
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97306336; PubMed=9162061;				
RA	Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,				
RA	Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,				
RA	Porter T.G., Truneh A., Young P.R.;				
RT	"A newly identified member of the tumor necrosis factor receptor				
RT	superfamily with a wide tissue distribution and involvement in				
RT	lymphocyte activation.";				
RL	J. Biol. Chem. 272:14272-14276(1997).				
[3]					
RP	SEQUENCE FROM N.A.				
RA	Zhang W., Wan T., Cao X.;				
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.				
[4]					
RP	SEQUENCE FROM N.A., AND VARIANTS ARG-17 AND ILE-241.				
RX	MEDLINE=21629477; PubMed=11756979;				
RA	Struyf F., Posavac C.M., Keyaerts E., Van Ranst M., Corey L.,				
RA	Spear P.G.;				
RT	"Search for polymorphisms in the genes for herpesvirus entry mediator,				
RT	Nectin-1, and Nectin-2 in immune seronegative individuals.";				
RL	J. Infect. Dis. 185:36-44(2002).				
[5]					
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Skin;				
RX	MEDLINE=22388257; PubMed=12477932;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Suetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Boraldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				

O35305	mus musculus
P83626	mus musculus
P41272	mus musculus
P20334	mus musculus
P25118	mus musculus
P50555	sus scrofa
O19131	bos taurus
P29934	rattus norv
Q60846	mus musculus
P28908	homo sapien
Q9er63	mus musculus
Q9er62	mus musculus

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hales S., Garcia A.M., Gay L.J., Rulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", *Proc. Natl. Acad. Sci. U.S.A.* 99:16899-16903 (2002).

[6]

INTERACTION WITH TRAF2 AND TRAF5.
MEDLINE=97298041; PubMed=9153189;
Hsu H., Solovyeve I., Colombero A., Elliott R., Kelley M., Boyle W.J., "ATAR, a novel tumor necrosis factor receptor family member, signals through TRAF2 and TRAF5.", *J. Biol. Chem.* 272:13471-13474 (1997).

[7]

INTERACTION WITH TRAF3 AND TRAF5.
MEDLINE=97306297; PubMed=9162022;
Mazsters S.A., Ayres T.M., Skubatch M., Gray C.L., Rothe M., Ashkenazi A., "Herpesvirus entry mediator, a member of the tumor necrosis factor receptor (TNFR) family, interacts with members of the TNFR-associated factor family and activates the transcription factors NF-kappaB and AP-1.", *J. Biol. Chem.* 272:14029-14032 (1997).

[8]

X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.
MEDLINE=21403268; PubMed=11511370;
Carfi A., Willis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H., Eisenberg R.J., Wiley D.C., "Herpes simplex virus glycoprotein D bound to the human receptor HveA.", *Mol. Cell* 8:169-179 (2001).

-!- FUNCTION: Receptor for TNFRSF14/LIGHT and homotrimeric TNFRSF1/lymphotoxin-alpha. Involved in lymphocyte activation. Plays an important role in HSV pathogenesis because it enhanced the entry of several wildtype HSV strains of both serotypes into CHO cells, and mediated HSV entry into activated human T cells.

-!- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5.

-!- SUBCELLULAR LOCATION: Type I membrane protein. (Probable).

-!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION IN LUNG, SPLEEN, AND THYMUS.

-!- SIMILARITY: Contains 3 TNFR-Cys repeats.

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EMBL; U70321; AAB58354.1; -.
EMBL; U81232; AAD00505.1; -.
EMBL; AF153378; AAF75588.1; -.
EMBL; AF373877; AAL47717.1; -.
EMBL; AF373878; AAL47718.1; -.
EMBL; BC002794; AAR02794.1; -.
PDB; 1JMA; 26-SEP-01.
Genew; HGNC:11912; TNFRSF14.
MIM; 602746; -.
GO; GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.
GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
GO; GO:0006955; P:immune response; TAS.
InterPro; IPR008063; Fas_receptor.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
PRINTS; PR01680; FASRECEPTOR.

DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00650; TNFR_NGFR_2; 2.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
KW 3D-structure.
FT SIGNAL 1 38 POTENTIAL.
FT CHAIN 39 283 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 39 202 SUPERFAMILY MEMBER 14.
FT TRANSMEM 203 223 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 224 283 POTENTIAL.
FT REPEAT 42 75 CYTOPLASMIC (POTENTIAL).
FT REPEAT 78 119 TNFR-CYS 1.
FT REPEAT 121 162 TNFR-CYS 2.
FT DISULFID 42 53 TNFR-CYS 3.
FT DISULFID 54 67
FT DISULFID 57 75
FT DISULFID 78 93
FT DISULFID 96 111
FT DISULFID 99 119
FT DISULFID 121 138
FT DISULFID 127 135
FT CARBOHYD 110 110
FT CARBOHYD 173 173
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FT VARIANT 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 241 241 K -> R (in dbSNP:4870).
FT VARIANT 241 241 /FTId=VAR_013007.
FT VARIANT 241 241 V -> I.
FT VARIANT 241 241 /FTId=VAR_013440.
FT TURN 44 45
FT STRAND 46 46
FT STRAND 49 49
FT TURN 50 51
FT STRAND 52 52
FT STRAND 55 55
FT STRAND 57 57
FT TURN 59 60
FT STRAND 61 65
FT STRAND 74 77
FT TURN 80 81
FT STRAND 82 83
FT STRAND 88 88
FT STRAND 94 95
FT TURN 101 104
FT STRAND 105 109
FT STRAND 118 121
FT TURN 123 124
FT STRAND 125 129
FT STRAND 137 140
SQ SEQUENCE 283 AA; 46CE13C2C70242C1 CRC64;
Query Match 92.2%; Score 1057; DB 1; Length 283;
Best Local Similarity 97.9%; Pred. No. 2.7e-80;
Matches 183; Conservative 2; Mismatches 0; Indels 2; Gaps 1;
QY 1 MEPPGDWGPFPWKESTRPTDVLRLVLYLTLFLGAPCYAPALPCKEDEVFVGSCECPKCSFG 60
Db 1 MEPPGDWGPFPWKESTRPTDVLRLVLYLTLFLGAPCYAPALPCKEDEVFVGSCECPKCSFG 60
QY 61 YRKEACGELTGVCEPCPPGTYIAHNLKLCLOQCDPAMGLRASNCRSTENAVCG 120
Db 61 YRKEACGELTGVCEPCPPGTYIAHNLKLCLOQCDPAMGLRASNCRSTENAVCG 120
QY 121 CSPGHFCIVQDGDHCAACRAYATSPGQGVKGGTSPQDTLCQNCPPGTFSPNGTLEECQ 180
Db 121 CSPGHFCIVQDGDHCAACRAYATSPGQGVKGGTSPQDTLCQNCPPGTFSPNGTLEECQ 180
QY 181 HOT--NW 185
Db 181 HQTCKSW 187

RESULT 2
CRME_CAMPS

```

Query Match      23.3%; Score 266.5; DB 1; Length 349;
Best Local Similarity 33.1%; Pred. No. 4.2e-15;
Matches 57; Conservative 24; Mismatches 76; Indels 15; Gaps 5;

21 LRVLVLTFLGAPC-----YAPALPCKEDEVFVGSCECPKCSGYRVKCAAGEL 70

```

DISULFID 86 104 BY SIMILARITY.
 DISULFID 106 120 BY SIMILARITY.
 DISULFID 123 146 BY SIMILARITY.
 DISULFID 129 149 BY SIMILARITY.
 DISULFID 164 185 BY SIMILARITY.
 CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SEQUENCE 325 AA; 35132 MW; 810530339198A71E CRC64;
 Query Match 22.8%; Score 261; DB 1; Length 325;
 Best Local Similarity 33.3%; Pred. No. 1.1e-14;
 Matches 58; Conservative 23; Mismatches 81; Indels 12; Gaps 6;
 20 VLRLVLYFLGAPFCYAPALP-----SKDEYFVSGCEPKSPGVRVKEACGELTGT 73
 1 MLRLIALLVCV-VYVYGDVPPVSSNQKGGHDYBKGLCCASCHPGFYASRLCGPGSNT 59
 74 VCBPCCPGTIVIAHLNGLSKLCQCMCDPAMG-LRASRNCSTENAVCGCPGHFCIVQDG 132
 60 VCSPCEDGTTASTNAPACVSCR--GPTGHLSESQPCDRTHDVCNCSGNGVCLLKGG 117
 133 DHMACRAYATSPGVRVKGSTESODILCQCPPTGTFSPN-GTLECCQHQTNW 195
 118 NGCRIC-APQTKPCAGYGVSGHTRAGDTLCEKCPHTYSDSLSPTRCGTSFNY 170

RESULT 4

1B HUMAN STANDARD; PRT; 461 AA.
 1 TR1B HUMAN STANDARD; PRT; 461 AA.
 2 P20333; Q16042; Q9U1H1;
 3 01-FEB-1991 (Rel. 17, Created)
 4 28-FEB-1991 (Rel. 41, Last sequence update)
 5 15-MAR-2004 (Rel. 43, Last annotation update)
 6 Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
 7 necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Etanercept)
 8 [Contains: Tumor necrosis factor binding protein 2 (TNFII)].
 9 TNFRSF1B OR TNFR2 OR TNFR.
 10 Homo sapiens (Human).
 11 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 12 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 13 NCBI_TaxID=9606;
 14 [1]
 15 SEQUENCE FROM N.A.
 16 MEDLINE=90260639; PubMed=2160731;
 17 A Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
 18 Dower S.K., Cosman D., Goodwin R.G.;
 19 "A receptor for tumor necrosis factor defines an unusual family of
 20 cellular and viral proteins.";
 21 Science 248:1019-1023(1990).
 22 [2]
 23 SEQUENCE FROM N.A., AND VARIANT ARG-196.
 24 MEDLINE=91045991; PubMed=2172983;
 25 A Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
 26 Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
 27 "A second tumor necrosis factor receptor gene product can shed a
 28 naturally occurring tumor necrosis factor inhibitor.";
 29 Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
 30 [3]
 31 SEQUENCE FROM N.A.
 32 MEDLINE=96299745; PubMed=8661109;
 33 A Beltonger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
 34 Lepaslier D., Scallard B.J., Goeddel D.V., Desauvage F.J.,
 35 Brodeur G.M.;
 36 "Physical mapping and genomic structure of the human TNFR2 gene.";
 37 Genomics 35:94-100(1996).
 38 [4]
 39 SEQUENCE FROM N.A., AND VARIANTS ARG-196; LYS-232; PRO-269 AND
 40 ARG-301.
 41 A Rieder M.J., Livingston R.J., Daniels M.P., Chung M.-W.,
 42 Miyamoto K.E., Nguyen C.P., Nguyen D.A., Foel C.L., Robertson P.D.,
 43 Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;

Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 [5]
 RN SEQUENCE FROM N.A.
 RC TISSUE=PNS;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.K., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cabant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Richards S., Worley K.C., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Fahey J., Heltan E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 37-461 FROM N.A.
 RX MEDLINE=91370690; PubMed=1966549;
 RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,
 RA Brockhaus M., Lesslauer W.;
 RT "Two human TNF receptors have similar extracellular, but distinct
 RT intracellular, domain sequences.";
 RL Cytokine 2:231-237(1990).
 RN [7]
 RP SEQUENCE OF 116-461 FROM N.A., PARTIAL SEQUENCE, AND VARIANT ARG-196.
 RX MEDLINE=90349572; PubMed=2166946;
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
 RA Ringold G.M.;
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor
 RT and demonstration of a shed form of the receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
 RN [8]
 RP SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.
 RX MEDLINE=21069356; PubMed=11197692;
 RA Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;
 RT "New single nucleotide polymorphisms in the coding region of human
 RT TNFR2: association with systemic lupus erythematosus.";
 RL Genes Immun. 1:501-503(2000).
 RN [9]
 RP SEQUENCE OF 27-31.
 RX MEDLINE=90110215; PubMed=2153136;
 RA Engelmann H., Novick D., Wallach D.;
 RT "Two tumor necrosis factor-binding proteins purified from human
 RT urine. Evidence for immunological cross-reactivity with cell surface
 RT tumor necrosis factor receptors.";
 RL J. Biol. Chem. 265:1531-1536(1990).
 RN [10]
 RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
 RX MEDLINE=91056048; PubMed=2173696;
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
 RA Brockhaus M.;
 RT "Purification and partial amino acid sequence analysis of two
 RT distinct tumor necrosis factor receptors from HL60 cells.";
 RL J. Biol. Chem. 265:20131-20138(1990).
 RN [11]
 RP CHARACTERIZATION.
 RX MEDLINE=93016040; PubMed=1328224;
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
 RA Lipari M.T., Goeddel D.V.;
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
 RT Characterization of ligand binding, internalization, and receptor
 RT phosphorylation.";
 RL J. Biol. Chem. 267:21172-21178(1992).

MEDLINE=95184010; PubMed=7533327;
Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
"Involvement of CRAPI1, a relative of TRAF, in CD40 signaling.";
Science 267:1494-1498(1995).
[6]
INTERACTION WITH TRAF5.
MEDLINE=96382484; PubMed=8790348;
Ishida T., Tolo T., Aoki T., Kobayashi N., Onishi T., Watanabe T.,
Yamamoto T., Inoue J.-I., et al. 1996.
TRAF5, a novel tumor necrosis factor receptor-associated factor
family protein, mediates CD40 signaling.";
Proc. Natl. Acad. Sci. U.S.A. 93:9437-9442 (1996).
-!- FUNCTION: Receptor for TNFSF5/CD40L.
-!- SUBUNIT: Interacts with TRAF3 and TRAF5. Interacts with TRAF1,
TRAF2 and TRAF6 (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms I, III, IV
and V); secreted (isoform II).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=5;
Name=I;
 IsoId=P27512-1; Sequence=Displayed;
Name=II;
 IsoId=P27512-2; Sequence=VSP_006474, VSP_006475;
Name=III;
 IsoId=P27512-3; Sequence=VSP_006477, VSP_006478;
Name=IV;
 IsoId=P27512-4; Sequence=VSP_006479, VSP_006480;
Name=V;
 IsoId=P27512-5; Sequence=VSP_006476;
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announcement/>
or send an email to license@isb-sib.ch).

EMBL; M83312; AAB08705.1; -;
EMBL; M94126; AAA37404.1; -;
EMBL; M94129; AAA37404.1; JOINED.
EMBL; M94128; AAA37404.1; JOINED.
EMBL; M94127; AAA37404.1; JOINED.
EMBL; AJ401387; CAC29427.1; -;
EMBL; AJ401388; CAC29428.1; -;
EMBL; AJ401389; CAC29429.1; -;
EMBL; AJ401390; CAC29430.1; -;
PIR; A46476; A46476.
HSP; P25942; ICDF.
MGD; MG1.88336; Tnfrsf5.
InterPro; IPR008063; Fas_receptor.
InterPro; IPR001368; TNFR_C6.
Pfam; PF00020; TNFR_C6; 4.
PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 4.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PSS0050; TNFR_NGFR_2; 4.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
Alternative splicing.
SIGNAL 1 19 POTENTIAL.
CHAIN 20 289 TUMOR NECROSIS FACTOR RECEPTOR
DOMAIN 20 193 SUPERFAMILY MEMBER 5.
DOMAIN 194 215 EXTRACELLULAR (POTENTIAL).
DOMAIN 216 289 POTENTIAL.
REPEAT 25 60 CYTOPLASMIC (POTENTIAL).
REPEAT 61 103 TNFR-CYS 1.
REPEAT 104 144 TNFR-CYS 2.
REPEAT 145 187 TNFR-CYS 3.
REPEAT 145 187 TNFR-CYS 4.
DISULFID 26 37 BY SIMILARITY.
DISULFID 38 51 BY SIMILARITY.
DISULFID 41 59 BY SIMILARITY.

Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownteen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Syamane N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitemead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;
"The DNA sequence and comparative analysis of human chromosome 20.";
Nature 414:865-871(2001).
[3]
SEQUENCE FROM N.A. (ISOFORM II).
MEDLINE=21117110; PubMed=1172023;
Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
"Regulation of CD40 function by its isoforms generated through alternative splicing.";
Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
[4]
SEQUENCE FROM N.A. (ISOFORM I).
TISSUE=Ovary;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Richards S., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W., Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.L., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
INTERACTION WITH TRAF3.
MEDLINE=95184010; PubMed=7533327;
Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
"Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";
Science 267:1494-1498(1995).
[6]
INTERACTION WITH TRAF3.
MEDLINE=95129692; PubMed=7530216;
Sato T., Irie S., Reed J.C.;
"A novel member of the TRAF family of putative signal transducing proteins binds to the cytosolic domain of CD40.";
FEBS Lett. 358:113-118(1995).
[7]
INTERACTION WITH TRAF3.
MEDLINE=98384149; PubMed=9718306;
Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J., Kehry M.R.;
"CD40-tumor necrosis factor receptor-associated factor (TRAF) interactions: regulation of CD40 signaling through multiple TRAF binding sites and TRAF hetero-oligomerization.";
Biochemistry 37:11836-11845(1998).
[8]
INTERACTION WITH TRAF5.
MEDLINE=98172745; PubMed=9511754;
Mizushima S.-I., Fujita M., Iehida T., Azuma S., Kato K., Hirai M., Otsuka M., Yamamoto T., Inoue J.-I.;
"Cloning and characterization of a cDNA encoding the human homolog of tumor necrosis factor receptor-associated factor 5 (TRAF5).";
Gene 207:135-140(1998).
[9]
INTERACTION WITH TRAF6.
MEDLINE=98095703; PubMed=9432981;
Kashiwada M., Shirakata Y., Inoue J.-I., Nakano H., Okazaki K., Okumura K., Yamamoto T., Nagaoka H., Takemori R.;
"Tumor necrosis factor receptor-associated factor 6 (TRAF6) stimulates extracellular signal-regulated kinase (ERK) activity in CD40 signaling along a ras-independent pathway.";
J. Exp. Med. 187:237-244(1998).
[10]
3D-STRUCTURE MODELING OF 24-144.
RP MEDLINE=97189482; PubMed=9037712;
Bajorath J., Aruffo A.;
"Construction and analysis of a detailed three-dimensional model of the ligand binding domain of the human B cell receptor CD40.";
Proteins 27:59-70(1997).
[11]
3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RP MEDLINE=98266353; PubMed=9605317;
Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M., Zheng Z., Naismith J.H., Thomas D.;
"The role of polar interactions in the molecular recognition of CD40L with its receptor CD40.";
Protein Sci. 7:1124-1135(1998).
[12]
X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH TRAF3.
RP MEDLINE=20442386; PubMed=10984535;
Ni C.Z., Welsh K., Leo E., Chieu C.K., Wu H., Reed J.C., Ely K.R.;
"Molecular basis for CD40 signaling mediated by TRAF3.";
Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).
[13]
X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH TRAF3.
RP MEDLINE=22000222; PubMed=12005438;
Li C., Ni C.Z., Havert M.L., Cabezas E., He J., Kaiser D., Reed J.C., Satterthwait A.C., Cheng G., Ely K.R.;
"Downstream regulator TANK binds to the CD40 recognition site on TRAF3.";
Structure 10:403-411(2002).
[14]
VARIANT HIGM3 ARG-83.
RP MEDLINE=21532985; PubMed=11675497;
Ferrari S., Gilliani S., Insalaco A., Al-Chonaim A., Soresina A.R., Loubser M., Avanzini M.A., Marconi M., Badolato R., Ugazio A.G., Levy I., Cacialan N., Durandy A., Takhia A., Notarangelo L.D., Plebani A.;
"Mutations of CD40 gene cause an autosomal recessive form of immunodeficiency with hyper IgM.";
Proc. Natl. Acad. Sci. U.S.A. 98:12614-12619(2001).
CC -!- FUNCTION: Receptor for TNFSF5/CD40L.
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform I); secreted (isoform II).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=I;
CC IsoId=P25942-1; Sequence=Displayed;
CC Name=II;
CC IsoId=P25942-2; Sequence=VSP 006472, VSP 006473;
CC -!- TISSUE SPECIFICITY: B-cells and in primary carcinomas.
CC -!- DISEASE: Defects in TNFSF5 are the cause of hyper-IgM immunodeficiency type 3 (HIGM3) [MIM:608843]. HIGM3 is an autosomal recessive disorder which includes an inability of B cells to undergo isotype switching, one of the final differentiation steps in the humoral immune system, an inability to mount an antibody-specific immune response, and a lack of germinal center formation.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".

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EMBL; X60592; CAA43045.1; -
EMBL; AL035662; CAC17670.1; -
EMBL; AJ300189; CAC29424.1; -
EMBL; BC012419; AHA12419.1; -
PIR; S04460; A60771.
PDB; 1CDF; 01-APR-97.
PDB; 1PLL; 18-OCT-00.
PDB; 1LOA; 08-FEB-00.
PDB; 1CZ2; 26-SEP-01.

Query Match 22.2%; Score 254; DB 1; Length 277;
Best Local Similarity 31.1%; Pred. No. 3.6e-14;
Matches 56; Conservative 30; Mismatches 78; Indels 16; Gaps 5;
20 VLRLVLYLTLFLGAPCVAPAL-----PSCKEDYVPGSECCPKCPGVRVKEACGELGTIV 74
1 MVLPLQCVLWG--CLLTVHPEPTACREKQYLINSQCCLCPGGKLVSDCTETETE 58
75 CBPCPPPTGYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCGSPGHFCIVQGDH 134
59 CLPQGESFELDTWNRETHCHQHKYCDPLGLRVQKGTSETDTICTCEGWHC---TSEA 115
135 CAACRAYATSSPGQVRQKGTESQTLQCNCPPTFS--PNGTLEECQHTQWPNHMECK 193
116 CESCVLHRSCTPGFGVQKQIATGSDTICEPCVPFFSNVSAFEKCHPWTG-----CETK 170

JULT 8
MB_COMPX
_CRMB_COMPX STANDARD; PRT; 351 AA.
OT3559; P87602;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Soluble TNF receptor II precursor (cytokine response modifying protein B).
(CRMB1 OR D2L) AND (CRMB2 OR I4R).
Cowpox virus (CPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
NCBI_TaxID=10243;
[1]
SEQUENCE FROM N.A.
STRAIN=GRI-90 / Grishak;
MEDLINE=98229462; PubMed=9568042;
Shchelkunov S.N., Saifonov P.F., Totmenin A.V., Petrov N.A.,
Ryzankina O.I., Gutorov V.V., Kotwal G.J.;
"The genomic sequence analysis of the left and right species-specific
terminal region of a cowpox virus strain reveals unique sequences and
a cluster of intact ORFs for immunomodulatory and host range
proteins.";
Virology 243:432-450(1998).
[2]
FUNCTION.
STRAIN=Brighton red;
MEDLINE=94378510; PubMed=8091665;
Hu P.O., Smith C.A., Pickup D.J.;
"Cowpox virus contains two copies of an early gene encoding a soluble
secreted form of the type II TNF receptor.";
Virology 204:343-356(1994).
-!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
the modification of TNF-mediated antiviral processes.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 2 TNFR-Cys repeats.

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EMBL; X94355; CAA64087.2; -
EMBL; X94355; CAD90756.1; -
HSSP; O14763; 1DOG.
InterPro; IPR001368; TNFR_C6.
Pfam; PF00202; TNFR_C6; 2.
SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00505; TNFR_NGFR_2; 2.
KW Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 19
FT CHAIN 20 351
FT REPEAT 31 67
FT REPEAT 69 110
FT REPEAT 32 43
FT DISULFID 44 57
FT DISULFID 47 67
FT DISULFID 70 85
FT DISULFID 88 102
FT DISULFID 92 110
FT CARBOHYD 103 103
FT CARBOHYD 191 191
FT CARBOHYD 250 250
SQ SEQUENCE 351 AA; 38253 MW; 57CAE73EF4ESD7C7 CRC64;

Query Match 21.2%; Score 243.5; DB 1; Length 351;
Best Local Similarity 31.0%; Pred. No. 3.3e-13;
Matches 54; Conservative 27; Mismatches 76; Indels 17; Gaps 6;
21 LRLVLYLTLFLGAPC-----YAPALPSCKEDYVPGSECCPKCPGVRVKEACGEL 70
1 MKSLVLYLTLFLSCIINGRDIAPHPNGKCKDNEVNRHNLCLSCPPTGYASRLCDCK 60
71 --TGTVCPCPPPTGYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCGSPGHFC 127
61 TMTNTQCTPCGGSGTFTSRNNHLPACLSCNGRCD--SNQVTRSCNTHNRCECAPGYVC 118
128 IVQGDHCAACRAYATSSPGQVRQKGTESQTLQCNCPPTFSN-GTLEECQ 180
119 LLKSGSGCKACVQKCGIGYV-SGHTSTGTVGVCSPGLGTYSHTVSSADKCE 171

RESULT 9
ID TNRS_BOVIN STANDARD; PRT; 269 AA.
AC Q28203;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
(CD40L receptor) (B-cell surface antigen CD40) (P-fragment).
GN TNFRSF5 OR CD40.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97281252; PubMed=9135560;
RA Hirano A., Brown W.C., Estes D.M.;
"Cloning, expression and biological function of the bovine CD40
homologue: role in B-lymphocyte growth and differentiation in
cattle.";
RL Immunology 90:294-300(1997).
CC -!- FUNCTION: Receptor for TNFSF5/CD40L.
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (by
similarity).

!!- SUBCELLULAR LOCATION: Type I membrane protein.
!!- SIMILARITY: Contains 4 TNFR-Cys repeats.

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EMBL: U57745; AAC48710.1; --
HSSP; P25942; 1CDF.
InterPro: IPR008063; Fas_receptor.
Pfam: PF001368; TNFR_c6.
PRINTS: PR01680; FASRECEPTOR.
SMART: SM00208; TNFR: 4.
PROSITE: PS00652; TNFR_NGFR_1; 1.
PROSITE: PS00500; TNFR_NGFR_2; 1.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
SIGNAL 1 19
CHAIN 20 >269
TUMOR NECROSIS FACTOR RECEPTOR
SUPERFAMILY MEMBER 5.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 180 269
NON_TER 269
SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;
Query Match 21.1%; Score 242; DB 1; Length 269;
Best Local Similarity 29.8%; Pred No. 3.4e-13;
Matches 53; Conservative 32; Mismatches 31; Indels 12; Gaps 4;
20 VRLVLYLTLFLG---APCYAPALPSCKEDEVYVSGECPCPKSGYRVKEACGELTGTVC 76
1 MVRPLQLFLWGFLLTAVHSEFATACGEKQYVNSLCCDLCPQCKLVNDCTEVSKTEQC 60
77 PCPPCTYIAHLNGLSKCIQCQCPDPMGLRASNCRSTENAVGCSFGHFCIVQDGDHCA 136
61 SGKGFEFLSTWNRKYCHEHYCPNGLRLQSGTLNTDTICVCEGQC---TSHTC 117
137 ACRAVATSPGQVKGSTESQDLCQCPPTGTS--PNTLEECQHOTNPWPMCRKK 193
118 SCTPHSLCLPGFGVQKIATGLDTCVCEPLGFTFSNVSSAFCKHRWTS-----CERK 170
STANDARD; PRT; 435 AA.

RESULT 10
TNFR3 HUMAN
P36941;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 3 precursor
(lymphotoxin-beta receptor) (tumor necrosis factor receptor 2 related protein) (tumor necrosis factor C receptor).
LTHR OR TNFRSF3 OR TNFR.
Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RX MEDLINE=93252381; PubMed=8486360;
RA Baers M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human l2p
transcribed sequences derived from a somatic cell hybrid.";
RL Genomics 16:214-218(1993).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RN FUNCTION.
RX MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., VanArsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RL Science 264:707-710(1994).
RN [4]
RN CHARACTERIZATION.
RX MEDLINE=99223511; PubMed=10207006;
RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
death in HeLa cells.";
RL J. Biol. Chem. 274:11868-11873(1999).
RN [5]
RN FUNCTION.
RX MEDLINE=20261554; PubMed=10799510;
RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
RA Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
RT "The lymphotoxin-beta receptor is necessary and sufficient for
LIGHT-mediated apoptosis of tumor cells.";
RL J. Biol. Chem. 275:14307-14315(2000).
RN [6]
RN INTERACTION WITH TRAF3.
RX MEDLINE=96278943; PubMed=8663299;
RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
RA Yagita H., Okumura K.;
RT "TRAF3, an activator of NF-kappaB and putative signal transducer for
the lymphotoxin-beta receptor.";
RL J. Biol. Chem. 271:14661-14664(1996).
RN [7]
RN INTERACTION WITH TRAF4.
RX MEDLINE=98289299; PubMed=9626059;
RA Krajewska M., Krajewski S., Zapata J.M., VanArsdale T.,
RA Gascoyne R.D., Berem K., McFadden D., Shabalik A., Hugh J.,
RA Reynolds A., Cleveland C.V., Reed J.C.;
RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal
adult, fetal, and tumor tissues.";

ry Match 20.9%; Score 239.5; DB 1; Length 435;
 t Local Similarity 28.3%; Pred. No. 8.8e-13;
 ches 75; Conservative 16; Mismatches 81; Indels 93; Gaps 13;
 4 PG-DKGPPWRTPRTDVLRLVLTFL-----GAPCYAPALPSCK--BDEY--PWGS 51
 10 PGLAWGP-----LVTLFGLLAASQVAPVPSAENGTCDQKNEYFQHR 56
 52 ECPKCSPGYRYKEAGBELTVCPECPPTTYIAHLNGLSKLCQCMCDPAMGLASRNC 111

RESULT 11

MEDLINE=99253915; PubMed=10318773;
 Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
 "A newly identified member of tumor necrosis factor receptor
 superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
 J. Biol. Chem. 274:13733-13736(1999).
 [3]
 SEQUENCE FROM N.A.
 TISSUE=Lung;
 MEDLINE=20122600; PubMed=1065513;
 Bai C., Connolly B., Metzger M.L., Hilliard C.A., Liu X., Sandig V.,
 Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
 "Overexpression of M68/DCR3 in human gastrointestinal tract tumors
 independent of gene amplification and its location in a four-gene
 cluster";
 Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
 [4]
 SEQUENCE FROM N.A.
 Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 [5]
 SEQUENCE FROM N.A.
 TISSUE=Lung and Skin;
 MEDLINE=2238257; PubMed=12477932;
 Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ustin T.B., Toshlyki S., Carlincl P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Rahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 -I- FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF14/LIGHT
 and TNFSF6/FasL. Protects against apoptosis.
 -I- SUBCELLULAR LOCATION: Secreted.
 -I- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.
 Detected in adult stomach, spinal cord, lymph node, trachea,
 spleen, colon and lung. Highly expressed in several primary tumors
 from colon, stomach, rectum, esophagus and in SW480 colon
 carcinoma cells.
 -I- SIMILARITY: Contains 4 TNFR-Cys repeats.

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 EMBL; AF104419; RAD03056.1; -
 EMBL; AF134240; RAD2688.1; -
 EMBL; AF217796; AAF3244.1; -
 EMBL; AF217793; AAF33685.1; -
 EMBL; AF217794; AAF33686.1; -
 EMBL; AL121845; CAC03668.1; -
 EMBL; BC017065; AAH17065.1; -
 EMBL; BC034349; AAH34349.1; -
 HSP; OA4763; IDO6; TNFRSF6B.
 Genew; HGNC:11921; TNFRSF6B.
 MIM; 603361; -
 GO; GO:0005625; C:soluble fraction; TAS.

DR GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0006916; P:anti-apoptosis; TAS.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF00020; TNFR_C6; 4.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00650; TNFR_NGFR_2; 2.
 KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 300
 TUMOR NECROSIS FACTOR RECEPTOR
 SUPERFAMILY MEMBER 6B.
 FT REPEAT 31 70
 FT TNFR-CYS 1.
 FT REPEAT 72 113
 FT TNFR-CYS 2.
 FT REPEAT 115 150
 FT TNFR-CYS 3.
 FT REPEAT 152 193
 FT TNFR-CYS 4.
 FT BY SIMILARITY.
 FT DISULFID 49 62
 FT BY SIMILARITY.
 FT DISULFID 52 70
 FT BY SIMILARITY.
 FT DISULFID 73 88
 FT BY SIMILARITY.
 FT DISULFID 91 105
 FT BY SIMILARITY.
 FT DISULFID 115 126
 FT BY SIMILARITY.
 FT DISULFID 132 150
 FT BY SIMILARITY.
 FT DISULFID 153 168
 FT BY SIMILARITY.
 FT DISULFID 174 193
 FT BY SIMILARITY.
 FT CARBOHYD 173 173
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 300 AA; 32679 MW; F90AEE33718449AF CRC64;
 Query Match 20.2%; Score 231; DB 1; Length 300;
 Best Local Similarity 35.8%; Pred. No. 3.1e-12;
 Matches 64; Conservative 15; Mismatches 78; Indels 22; Gaps 8;
 QY 16 PRDVLRLVLTFLGAPCYAPALPSCKE-DEYP-----VGSE-CCPKCSPGYRKEACG 68
 DB 7 PGLSLLCLVLPAL---LPVAVGVVAETTYPRDAETGERLVCAQCPGTFVQRPGR 63
 QY 69 ELTGVNCPGPGTGVIAHLNGLSKLQCCQMDPAMGLR--ASRNCSTENAVCCSPGHF 126
 DB 64 RDSPTTCGCPPRHYTQFWNYLER---CRYCNVLGGEERAEARACHATHNACRCRTGFF 120
 QY 127 CIVQGDHCAACRAVATSSPGQVKGTSSQDTLCQNCPPGTFSPNGTLEECQHTN 184
 DB 121 A-----HAGFCLERHASCPPAGVIAPGTPSQNTCCQCPPTFSASSSSSEQCPHRN 173
 RESULT 14
 TR16 MOUSE
 ID TR16 MOUSE STANDARD; PRT; 417 AA.
 AC Q9Z0F1;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-
 affinity nerve growth factor receptor) (NGF receptor) (Low affinity
 neurotrophin receptor p75NTR).
 GN NGFR OR TNFRSF16.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=A.
 RX MEDLINE=99077793; PubMed=9857182;
 RA Tuffereau C., Benejean J., Blondel D., Kieffer B., Flamand A.;
 "Low-affinity nerve-growth factor receptor (p75NTR) can serve as a
 receptor for rabies virus";
 RL EMBO J. 17:7250-7259(1998).
 CC -I- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
 AND NT-4. Can mediate cell survival as well as cell death of
 neural cells (By similarity). Binds to rabies virus glycoprotein
 Gs.
 CC -I- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-

Search completed: June 10, 2004, 12:32:27
Time : 39 secs

GenCore version 5.1.6
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protein - protein search, using sw model

on: June 10, 2004, 12:02:03 ; Search time 80 Seconds
(without alignments)
776.964 Million cell updates/sec

le: US-09-934-289A-18

quence: 1 MBPPGDWGPWRPRTDV.....BCQHTNPNHMCCKKAKG 197

ring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

arched: 1017041 seqs, 315518202 residues

tal number of hits satisfying chosen parameters: 1017041

imum DB seq length: 0

ximum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase : SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_veterebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query %	Length	ID	Description
1	920.5	80.3	283	6 Q9XSZ8	Q9XSZ8 cercopithec
2	552	48.2	273	11 Q80W99	Q80W99 mus musculu
3	460	40.1	199	4 Q8N634	Q8N634 homo sapien
4	323	28.2	136	11 Q8VC17	Q8VC17 mus musculu
5	292	25.5	278	6 Q8SQ34	Q8SQ34 sus scrofa
6	272	23.7	483	13 Q800K7	Q800K7 paralichthy
7	270.5	23.6	348	12 Q800K7	Q800K7 monkeyppox v
8	270.5	23.6	348	12 Q800K7	Q800K7 monkeyppox v
9	270.5	23.6	349	12 Q800K7	Q800K7 monkeyppox v
10	268.5	23.4	349	12 Q800K7	Q800K7 monkeyppox v
11	268.5	23.4	349	12 Q800K7	Q800K7 monkeyppox v
12	268.5	23.4	349	12 Q800K7	Q800K7 monkeyppox v
13	266.5	23.3	349	12 Q800K7	Q800K7 monkeyppox v
14	266.5	23.3	349	12 Q800K7	Q800K7 monkeyppox v
15	266.5	23.3	349	12 Q800K7	Q800K7 monkeyppox v
16	264.5	23.1	349	12 Q800K7	Q800K7 monkeyppox v

Q805b0 gallus gall
O57097 camelpox vi
Q8K2x6 mus musculu
O57117 cowpox viru
Q9Jke0 rattus norv
O57112 variola vir
Q8eyK5 homo sapien
O57111 variola vir
O57110 variola vir
Q80sr3 variola vir
O57109 variola vir
O57116 cowpox viru
Q8wmq2 ovis aries
O57121 cowpox viru
Q7tfh9 rhesus cyto
O57305 cowpox viru
O57122 cowpox viru
O57119 cowpox viru
O57120 cowpox viru
O57118 cowpox viru
Q8dgn7 gallus gall
Q7t2h3 oncorhynchu
O57123 cowpox viru
Q7yrl5 canis fami
O57115 cowpox viru
Q85308 cowpox viru
Q8dgn8 gallus gall
Q800i0 gallus gall
O02764 oryctolagus

ALIGNMENTS

RESULT 1

Q9XSZ8 PRELIMINARY; PRT; 283 AA.
ID O9XSZ8
AC O9XSZ8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE HveAs.
GN HVEAS.
OC Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=99256730; PubMed=10366573;
RA Foster T.P., Chouljenko V.N., Kousoulas K.G.;
RT "Functional characterization of the HveA homolog specified by African
RT green monkey kidney cells with a herpes simplex virus expressing the
RL green fluorescence protein.";
RL Virology 258:365-374(1999).
DR EMBL; AF147720; AAD37381.1; --
DR HSP; Q92956; 1JMA.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0004888; F.transmembrane receptor activity; IEA.
DR GO; GO:0006915; P.apoptosis; IEA.
DR GO; GO:0006955; P.immune response; IEA.
DR GO; GO:0007165; P.signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
DR PROSITE; PS00650; TNFR_NGFR_2; 2.
SQ SEQUENCE 283 AA; 30199 MW; 397951C6617FB3AA CRC64;

Query Match 80.3%; Score 920.5; DB 6; Length 283;
 Best Local Similarity 82.3%; Pred. No. 8.6e-88;
 Matches 158; Conservative 9; Mismatches 20; Indels 5; Gaps 1;

1 MEPPGDGPPWRSTPRDVLRLVLYTLFLGAPYAPALPSCKEDEYFVGSCECCPKCSPG 60
 1 MEPPGWSGPPRRAPKADILTLVLYTLFLGSSCYAPALPSCKEDEYFVGSCECCPKCSPG 60
 61 YRVKACGELTGTVCBPCPGTYIAHNLGSLKLCQCMCDPAMGLRASRNCSTENAVCG 120
 61 PHVRACGEQGTGTVCPCSPGTIAHNLGSLKLCQCMCDPAMGLRSTNCSTTANALCG 120
 121 CSPGHFCIVODGDHCAACRAYATSSPGQVKGSTESQDTLQNCPPGTFSPNGTLEECQ 180
 121 CSPGHFCIVODGDHCAACRAYATSSPGQVKGSTESQDTLQNCPPGTFSPNGTLEECQ 180
 181 HQTWPNHMCCK 192
 181 H-----GNKCSK 187

RESULT 2
 10WMS
 Q80WM9 PRELIMINARY; PRT; 275 AA.
 01-JUN-2003 (TrEMBLrel. 24, Created)
 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 Tumor necrosis factor receptor superfamily member 14 precursor.
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=C57BL/6; TISSUE=Thymus;
 Benencia F., Conejo-Garcia J.R., Courreges M.C., Coukos G.;
 "Light regulation in a murine model of ovarian carcinoma."
 Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 EMBL; AY264405; AAC09081.1;
 GO; GO:0016020; C:membrane; IEA.
 GO; GO:0004888; F:transmembrane receptor activity; IEA.
 GO; GO:0006915; P:apoptosis; IEA.
 GO; GO:0006955; P:immune response; IEA.
 GO; GO:0007165; P:signal transduction; IEA.
 InterPro; IPR008063; Fas receptor.
 Pfam; PF00020; TNFR_c6; 4.
 PRINTS; PR01680; FASRECEPTOR.
 SMART; SM00208; TNFR; 4.
 PROSITE; PS00652; TNFR_NGFR_1; 1.
 PROSITE; PS50050; TNFR_NGFR_2; 3.
 V Receptor; Signal.
 SIGNAL 1 38 Potential.
 SEQUENCE 275 AA; 30171 MW; C4A7EAD8EFC0521D CRC64;

Query Match 48.2%; Score 552; DB 11; Length 275;
 Best Local Similarity 53.3%; Pred. No. 2.1e-49;
 Matches 98; Conservative 18; Mismatches 68; Indels 0; Gaps 0;

1 MEPPGDGPPWRSTPRDVLRLVLYTLFLGAPYAPALPSCKEDEYFVGSCECCPKCSPG 60
 1 MEPLFCGWSGAPNSQAFDTNTFLVPCVFLNLLQRIASQPSRCRQEEFLVGECCPMCNPG 60
 61 YRVKACGELTGTVCBPCPGTYIAHNLGSLKLCQCMCDPAMGLRASRNCSTENAVCG 120
 61 YHVQVCSHTGTVCAPCPQTYIAHNLGSLKLCQCMCDPAMGLRASRNCSTENAVCG 120
 121 CSPGHFCIVODGDHCAACRAYATSSPGQVKGSTESQDTLQNCPPGTFSPNGTLEECQ 180
 121 CIPGYFCENQDSHSGSTCLQHTTCPPGQVKGSTESQDTLQNCPPGTFSPNGTLEECQ 180
 181 HQTWPNHMCCK 192

Db 181 PWTN 184

RESULT 3
 C8N634 PRELIMINARY; PRT; 199 AA.
 ID Q8N634
 AC Q8N634
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Similar to tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Lung;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC029848; AAH29848.1;
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001368; TNFR_c6;
 DR Pfam; PF00020; TNFR_c6; 1.
 KW Receptor.
 SQ SEQUENCE 199 AA; 21404 MW; F04A2264BC16D00A CRC64;
 Query Match 40.1%; Score 460; DB 4; Length 199;
 Best Local Similarity 95.4%; Pred. No. 5.9e-40;
 Matches 83; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 101 FAMGLRASRNCSTENAVCGSPGHFCIVODGDHCAACRAYATSSPGQVKGSTESQDT 160
 17 FAMGLRASRNCSTENAVCGSPGHFCIVODGDHCAACRAYATSSPGQVKGSTESQDT 76
 QY 161 LCQNCPPGTFSPNGTLEECQHOT--NW 195
 77 LCQNCPPGTFSPNGTLEECQHOTKCSW 103

RESULT 4
 Q8VC17 PRELIMINARY; PRT; 196 AA.
 ID Q8VC17
 AC Q8VC17
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC022125; AAH22125.1;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR008063; Fas receptor.
 DR InterPro; IPR001368; TNFR_c6;
 DR Pfam; PF00020; TNFR_c6; 3.
 DR PRINTS; PR01680; FASRECEPTOR.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS50050; TNFR_NGFR_2; 1.
 KW Hypothetical protein.
 FT NON_TER 1

```

SEQUENCE 196 AA; 21555 MW; 2AB3FF8905E260B8 CRC64;
Query Match 28.2%; Score 323; DB 11; Length 196;
est Local Similarity 56.3%; Pred. No. 1.1e-25;
atches 58; Conservative 10; Mismatches 35; Indels 0; Gaps 0;

82 TYIAHLNGLSKLQCCQDCDPAMGLRASNCRSTENAVCGSPGHFCIVQDGHCAACRAY 141
2 TYTAHANGSLKLPVGGVCDPMGLLTWQECSSWXTVCRCPGFCENQDGHSCSTCLOH 61
142 ATSSPGQVQKGTSTESQDILQCNCPGPFNSPGLTLEECQHTN 184
62 TTCPPQQRVEKGTHTDQTVACDLCTGTSLGTTQEECLPWN 104

ULT 5
Q34
Q8SQ34 PRELIMINARY; PRT; 278 AA.
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 21, Last annotation update)
CD40.
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
[1]
SEQUENCE FROM N.A.
West K.A., Li A.W., Rowden G.;
"Characterization of the Porcine CD40 Molecule.";
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AF248545; AAL92924.1; -
GO; GO:0015020; C:membrane; IEA.
GO; GO:0004888; P:transmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008063; Fas receptor.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 4.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS00050; TNFR_NGFR_2; 4.
SEQUENCE 278 AA; 30951 MW; 20D446E44AF93DD2 CRC64;

Query Match 25.5%; Score 292; DB 6; Length 278;
est Local Similarity 36.2%; Pred. No. 2.7e-22;
atches 63; Conservative 25; Mismatches 76; Indels 10; Gaps 4;

21 LRLVLYLFLGAPCVAPALPSCKEDEYVGVSECCPKSPGYRVKAEGLTGTVCPCPP 80
6 LKCLLWGCFLLAVHEPP-TCSENQVFTNSRCCNLCPFGQKLVNHTVETETELPCSS 64
81 GYIAHLNGLSKLQCCQDCDPAMGLRASNCRSTENAVCGSPGHFCIVQDGHCAACRA 140
65 SEFLATWNRKHCHQKCYCDENLGLQVREGTSKTDITCVCSGHHG---TNSACSECTL 121
141 YATSSPGQVQKGTSTESQDILQCNCPPTFS-PNGTLEECQHTNWNHMCCK 193
122 HSLCPFLGLVKQMATEVSDTICEPCPVGFNFNSASEKQPTWS-----CESK 170

ULT 6
OK7
Q800K7 PRELIMINARY; PRT; 483 AA.
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Tumor necrosis factor receptor-2.
TNFR-2.

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```

OS Paralichthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralichthyidae; Paralichthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Park C., Kurobe T., Hirono I., Aoki T.;
RT "Cloning and characterization of cDNAs for two distinct tumor necrosis
RT factor receptor superfamily genes from Japanese flounder Paralichthys
RT olivaceus.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB080947; BAC65226.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6; 3.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
KW Receptor.
SQ SEQUENCE 483 AA; 52227 MW; BE55874A8C7F2085 CRC64;

Query Match 23.7%; Score 272; DB 13; Length 483;
est Local Similarity 36.9%; Pred. No. 5.8e-20;
Matches 52; Conservative 18; Mismatches 69; Indels 2; Gaps 2;

QY 46 EYFVSECCPKSPGYRVKAEGLTGTVCPCPPGTYYIAHLNGLSKLQCCQDCDPAMGL 105
DB 33 EYREQDLCKKCPFGQLIKQSDATESVCKQDSGGYMEKNYAKLSCNKKNGKL 92
QY 106 RASRNCSTENAVCGSPGHFCIVQ-DGDHCAACRAYATSSPGQVQKGTSTESQDILQCN 164
DB 93 QYAEQCSSTFTGCVCKPGMYCIMDFNPYCASCENYSQCRAGVGSLPGKANSVKCEL 152
QY 165 CPPGTFS-PNGTLEECQHTN 184
DB 153 CPDGMFNTSNTTETCRPTD 173

RESULT 7
OS7108 PRELIMINARY; PRT; 348 AA.
ID OS7108;
AC OS7108;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Zaire-1970;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
RT orthopoxviruses to a particular species.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88142; AB594367.1; -
DR HSP; Q92856; LUMA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 348 AA; 38212 MW; BE55979057DEC91P CRC64;

Query Match 23.6%; Score 270.5; DB 12; Length 348;
est Local Similarity 32.4%; Pred. No. 5.9e-20;

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51  TINTOCTCGSDTFTSHNNHLOACLSCNGRCD--SNQVETRSCNTHNRIECSPGYICLL 118
130 QGDGPHCAACRAYATSPGQVQKGTGESQDILCQNCPPGTGTSFN- GTLEBCQHQTN 184
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
119 KGSSGCRCTCISKTKCGIGYGV-SGYTSTGDVICSPCGGTYSHTVSTDKCEPVT 173
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
057100 PRELIMINARY; PRT; 349 AA.
ID OS7100
AC OS7100;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
CMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
NCBI_TaxID=10244;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Nigeria-1971;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
RL orthopoxviruses to a particular species.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87844; AB94361.1; -.
DR HSSP; Q92356; LUNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
XW
SQ SEQUENCE 349 AA; 38239 MW; DF6C280D478F2422 CRC64;

Query Match 23.6%; Score 270.5; DB 12; Length 349;
Best Local Similarity 32.6%; Pred. No. 5.9e-20;
Matches 56; Conservative 26; Mismatches 75; Indels 15; Gaps 5;

QY 21 LRLVLYITFGAPC-----YAPALPCKEDEYFVGECEPKSPGYRVKEACGEL 70
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MRSVLYSILFLSCIINGRDIAHPASNGKCKDEYRNLCLCLCPPGGYASRLCDSK 60
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 71 TGTVCPECPGTVIAHLGSLKCLQO-MCDPAMGLRASRCSTENAVCCSPGFHCIV 129
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 TINTOCTCGSDTFTSHNNHLOACLSCNGRCD--SNQVETRSCNTHNRIECSPGYICLL 118
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 130 QGDGPHCAACRAYATSPGQVQKGTGESQDILCQNCPPGTGTSFN- GTLEBCQ 180
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 KGASGCRCTCISKTKCGIGYGV-SGYTSTGDVICSPCGGTYSHTVSTDKCE 169
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
057101 PRELIMINARY; PRT; 349 AA.
ID OS7101
AC OS7101;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
CMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
NCBI_TaxID=10244;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=zaire-1977;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the

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orthopoxviruses to a particular species";
Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
EMBL; U87845; AAB94362.1; -.
HSP; Q92956; 1JMA.

GO: GO:0004872; F:receptor activity; IEA.

InterPro; IPR001368; TNFR_c6.

SMART; SM00208; TNFR; 2.

PROSITE; PS00652; TNFR_NGFR_1; 2.

PROSITE; PS00500; TNFR_NGFR_2; 2.

Receptor.

SEQUENCE 349 AA; 38311 MW; 02F65B00CFB858BE CRC64;

Query Match 23.4%; Score 268.5; DB 12; Length 349;

Best Local Similarity 32.6%; Pred. No. 9.6e-20;

Matches 56; Conservative 25; Mismatches 76; Indels 15; Gaps 5;

21 LRLVLYTLFLGAPC-----YAPALPSCKEDYFVSGECCKPKSPGYRVKAEAGEL 70

1 MRSVLYSYILFLSCIIINGRDIAHPNSGKCKDNEYRSNLCCLSCPPGYASRLCDISK 60

71 TGTVCPCPPGTYIAHLNGLSKLQCC-MCDPAMGLASRNCSTENAVCCSPGHFCIV 129

61 TINTQCTPCGSDTFTSHNNHLOACLSCNGRCD--SNQVETRSCNTHNRICSPGYCYLL 118

130 QGDHCAACRAVATSSPGORVQKGTESQDTLCQNCPPGTSPN-GTLEECQ 180

119 KGSSGRTCTISKTKGIGYGV-SGYTSTGDIVCSFGPGTYSHVSTDKCE 169

SULT 11

7102

OS71102 PRELIMINARY; PRT; 349 AA.

01-JUN-1998 (TrEMBLrel. 06, Created)

01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

tumor necrosis factor receptor II homolog.

CRMB.

Monkeypox virus.

Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

Orthopoxvirus.

NCBI_TaxID=10244;

[1]

SEQUENCE FROM N.A.

Loparev V.N., Parsons J.M., Esposito J.J.;

"DNA sequence analysis as a criterion for allocation of the

orthopoxviruses to a particular species";

Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

EMBL; U87845; AAB94363.1; -.
HSP; Q92956; 1JMA.

GO: GO:0004872; F:receptor activity; IEA.

InterPro; IPR001368; TNFR_c6.

SMART; SM00208; TNFR; 2.

PROSITE; PS00652; TNFR_NGFR_1; 2.

PROSITE; PS00500; TNFR_NGFR_2; 2.

Receptor.

SEQUENCE 349 AA; 38308 MW; CBD2C949F994C59C CRC64;

Query Match 23.4%; Score 268.5; DB 12; Length 349;

Best Local Similarity 32.6%; Pred. No. 9.6e-20;

Matches 56; Conservative 25; Mismatches 76; Indels 15; Gaps 5;

21 LRLVLYTLFLGAPC-----YAPALPSCKEDYFVSGECCKPKSPGYRVKAEAGEL 70

1 MRSVLYSYILFLSCIIINGRDIAHPNSGKCKDNEYRSNLCCLSCPPGYASRLCDISK 60

71 TGTVCPCPPGTYIAHLNGLSKLQCC-MCDPAMGLASRNCSTENAVCCSPGHFCIV 129

61 TINTQCTPCGSDTFTSHNNHLOACLSCNGRCD--SNQVETRSCNTHNRICSPGYCYLL 118

QY 130 QGDHCAACRAVATSSPGORVQKGTESQDTLCQNCPPGTSPN-GTLEECQ 180

Db 119 KGSSGRTCTISKTKGIGYGV-SGYTSTGDIVCSFGPGTYSHVSTDKCE 169

RESULT 12

OS7291

ID 057291 PRELIMINARY; PRT; 349 AA.

AC 057291; (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Tumor necrosis factor receptor II homolog.

CRMB.

OS Monkeypox virus.

Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

Orthopoxvirus.

NCBI_TaxID=10244;

[1]

SEQUENCE FROM N.A.

RC STRAIN=VARIOUS STRAINS;

RA Loparev V.N., Parsons J.M., Esposito J.J.;

Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

EMBL; U88144; AAB94368.1; -.
EMBL; U87842; AAB94359.1; -.
EMBL; U87994; AAB94365.1; -.
EMBL; U87995; AAB94366.1; -.
EMBL; U88143; AAB94368.1; -.
HSP; Q92956; 1JMA.

GO: GO:0004872; F:receptor activity; IEA.

InterPro; IPR001368; TNFR_c6.

SMART; SM00208; TNFR; 2.

PROSITE; PS00652; TNFR_NGFR_1; 2.

PROSITE; PS00500; TNFR_NGFR_2; 2.

SEQUENCE 349 AA; 38295 MW; CBD2C949ED2B8E7C CRC64;

Query Match 23.4%; Score 268.5; DB 12; Length 349;

Best Local Similarity 32.6%; Pred. No. 9.6e-20;

Matches 56; Conservative 25; Mismatches 76; Indels 15; Gaps 5;

21 LRLVLYTLFLGAPC-----YAPALPSCKEDYFVSGECCKPKSPGYRVKAEAGEL 70

1 MRSVLYSYILFLSCIIINGRDIAHPNSGKCKDNEYRSNLCCLSCPPGYASRLCDISK 60

71 TGTVCPCPPGTYIAHLNGLSKLQCC-MCDPAMGLASRNCSTENAVCCSPGHFCIV 129

61 TINTQCTPCGSDTFTSHNNHLOACLSCNGRCD--SNQVETRSCNTHNRICSPGYCYLL 118

QY 130 QGDHCAACRAVATSSPGORVQKGTESQDTLCQNCPPGTSPN-GTLEECQ 180

Db 119 KGSSGRTCTISKTKGIGYGV-SGYTSTGDIVCSFGPGTYSHVSTDKCE 169

RESULT 13

OS7103

ID 057103 PRELIMINARY; PRT; 348 AA.

AC 057103; (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Tumor necrosis factor receptor II homolog.

CRMB.

OS Monkeypox virus.

Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

Orthopoxvirus.

NCBI_TaxID=10244;

[1]

SEQUENCE FROM N.A.

RC STRAIN=Zaire-1979;

RA Loparev V.N., Parsons J.M., Esposito J.J.;

"DNA sequence analysis as a criterion for allocation of the

orthopoxviruses to a particular species";

Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

1 EMBL; U87847; AAB94364.1; -;
2 HSP; Q92956; 1JMA.
3 GO: GO:0004872; F:receptor activity; IEA.
4 InterPro; IPR001368; TNFR_c6.
5 Pfam; PF00020; TNFR_c6; 2.
6 SMART; SM00208; TNFR; 2.
7 PROSITE; PS00652; TNFR_NGFR_1; 2.
8 PROSITE; PS50050; TNFR_NGFR_2; 2.
9 Receptor.
10 SEQUENCE 348 AA; 38184 MW; 34A5E668B27907B5 CRC64;

Query Match 23.3%; Score 266.5; DB 12; Length 348;
Best Local Similarity 33.1%; Pred. No. 1.5e-19;
Matches 56; Conservative 26; Mismatches 79; Indels 15; Gaps 5;
21 LRLVLYLFLGAPC-----YAPALPSCKEDEYPVGSCECPKSPGYRVEACGEL 70
1 MSALYLYLFLSCIIINGRDVTPYAPSGKCKDNEYKRNLCCLSCPPGTYSRLCDISK 60
71 TGTVCPCPPGTIAHLNGLSKLQCC-MCDPAMGLASRNCSTENAVCGSPGHFCIV 129
61 TMTQCTPCGSGTFTSRNNHLPACLSGRCDC--SNQVETRSCNTHNRICECSPGYCYIL 118
130 QGDHCAACRAYATSSPGQVQKGTESQDTLCQCPPTGTFSPN-GTLEECQ 180
119 KGSSGCKACVSTQKCGIGYV-SGHTSAGDVICSPGGLGTVSRTVSSADKCE 169

RESULT 14
57098 PRELIMINARY; PRT; 349 AA.

01-JUN-1998 (TREMBLrel. 06, Created)
01-JUN-1998 (TREMBLrel. 06, Last sequence update)
01-JUN-2003 (TREMBLrel. 24, Last annotation update)
Tumor necrosis factor receptor II homolog.

CRMB.
Camelpox virus (strain CP-1).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
NCBI_TaxID=203174;

SEQUENCE FROM N.A.
STRAIN=Saadi-M3;
Loparev V.N., Parsons J.M., Esposito J.J.;
"DNA sequence analysis as a criterion for allocation of the
orthopoxviruses to a particular species";
Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

1 EMBL; U87839; AAB94356.1; -;
2 HSP; Q92956; 1JMA.
3 GO: GO:0004872; F:receptor activity; IEA.
4 InterPro; IPR001368; TNFR_c6.
5 Pfam; PF00020; TNFR_c6; 2.
6 SMART; SM00208; TNFR; 2.
7 PROSITE; PS00652; TNFR_NGFR_1; 2.
8 PROSITE; PS50050; TNFR_NGFR_2; 2.
9 Receptor.
10 SEQUENCE 349 AA; 37978 MW; 8630EFAED7A584B5 CRC64;

Query Match 23.3%; Score 266.5; DB 12; Length 349;
Best Local Similarity 33.1%; Pred. No. 1.5e-19;
Matches 57; Conservative 24; Mismatches 76; Indels 15; Gaps 5;

21 LRLVLYLFLGAPC-----YAPALPSCKEDEYPVGSCECPKSPGYRVEACGEL 70
1 MSALYLYLFLSCIIINGRDVTPYAPSGKCKDNEYKRNLCCLSCPPGTYSRLCDISK 60
71 TGTVCPCPPGTIAHLNGLSKLQCC-MCDPAMGLASRNCSTENAVCGSPGHFCIV 129
61 TMTQCTPCGSGTFTSRNNHLPACLSGRCDC--SNQVETRSCNTHNRICECSPGYCYIL 118
130 QGDHCAACRAYATSSPGQVQKGTESQDTLCQCPPTGTFSPN-GTLEECQ 180

119 KGSSGCKACVSTQKCGIGYV-SGHTSAGDVICSPGGLGTVSRTVSSADKCE 169

RESULT 15

057284 PRELIMINARY; PRT; 349 AA.
AC 057284;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
CN CRMB

Camelpox virus (strain CP-1).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
NCBI_TaxID=203174;

SEQUENCE FROM N.A.
STRAIN=DUBAI-1992 / CP-5, and SOMALIA-1978;
Loparev V.N., Parsons J.M., Esposito J.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
EMBL; U87840; AAB94357.1; -;
EMBL; U87837; AAB94354.1; -;

HSP; Q92956; 1JMA.
GO: GO:0004872; F:receptor activity; IEA.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.

SEQUENCE 349 AA; 38036 MW; EA412AER86E090E4 CRC64;
Query Match 23.3%; Score 266.5; DB 12; Length 349;
Best Local Similarity 33.1%; Pred. No. 1.5e-19;
Matches 57; Conservative 24; Mismatches 76; Indels 15; Gaps 5;

21 LRLVLYLFLGAPC-----YAPALPSCKEDEYPVGSCECPKSPGYRVEACGEL 70
1 MSALYLYLFLSCIIINGRDVTPYAPSGKCKDNEYKRNLCCLSCPPGTYSRLCDISK 60
71 TGTVCPCPPGTIAHLNGLSKLQCC-MCDPAMGLASRNCSTENAVCGSPGHFCIV 129
61 TMTQCTPCGSGTFTSRNNHLPACLSGRCDC--SNQVETRSCNTHNRICECSPGYCYIL 118
130 QGDHCAACRAYATSSPGQVQKGTESQDTLCQCPPTGTFSPN-GTLEECQ 180
119 KGSSGCKACVSTQKCGIGYV-SGHTSAGDVICSPGGLGTVSRTVSSADKCE 169

Search completed: June 10, 2004, 12:34:03
Job time : 83 secs

GenCore version 5.1.6
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nucleic - nucleic search, using sw model

on: June 10, 2004, 07:19:52 ; Search time 2480 Seconds
(without alignments)
10328.925 Million cell updates/sec

le: US-09-934-289a-19
fect score: 591
quence: 1 agggagctctctggagactg.....aaaagaagaagccaaagggg 591

ring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

arched: 3470272 seqs, 21671516995 residues

al number of hits satisfying chosen parameters: 6940544

imum DB seq length: 0
timum DB seq length: 2000000000

it-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

abase :

GenEmbl:*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sta.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.ste.*
28: em.un.*
29: em.vi.*
30: em.htg.hum.*
31: em.htg.inv.*
32: em.htg.other.*
33: em.htg.mus.*
34: em.htg.pin.*
35: em.htg.rod.*
36: em.htg.mam.*
37: em.htg.vrt.*
38: em.sy.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB ID	Description
1	591	100.0	591	6	AR168183 Sequence
2	591	100.0	591	6	BD244691 Novel mol
3	591	100.0	1596	6	AR168182 Sequence
4	591	100.0	1596	6	BD244690 Novel mol
5	552.6	93.5	4622	6	AR169917 Sequence
6	552.6	93.5	4622	6	AR172621 Sequence
7	552.6	93.5	4622	6	AR340583 Sequence
8	550.8	93.2	831	6	BD244703 Novel mol
9	550.8	93.2	852	9	AF373878 Homo sapi
10	550.8	93.2	927	6	BD091696 HVM pol
11	550.8	93.2	1049	9	AY358879 Homo sapi
12	550.8	93.2	1612	9	BC002794 Homo sapi
13	550.8	93.2	1724	6	AR169913 Sequence
14	550.8	93.2	1724	6	AR173617 Sequence
15	550.8	93.2	1724	6	BD244687 Novel mol
16	550.8	93.2	1724	6	AR340579 Sequence
17	550.8	93.2	1724	6	AX700436 Sequence
18	550.8	93.2	1724	6	AX816347 Sequence
19	550.8	93.2	1724	9	HSU70321 Human herpe
20	550.8	93.2	1834	6	BD244702 Novel mol
21	550.8	93.1	579	6	AR168180 Sequence
22	550	93.1	579	6	BD244682 Novel mol
23	550	93.1	1815	6	AX427500 Sequence
24	550	93.1	1929	6	AR168179 Sequence
25	550	93.1	1929	6	BD244681 Novel mol
26	549.2	92.9	852	9	AF373877 Homo sapi
27	549.2	92.9	881	6	BD260145 Human tum
28	549.2	92.9	1704	6	BD260131 Human tum
29	548.4	92.8	558	6	BD244697 Novel mol
30	548.4	92.8	2313	6	BD244696 Novel mol
31	547.6	92.7	1681	9	AF153978 Homo sapi
32	547.6	92.7	1704	6	AX022023 Sequence
33	547.6	92.7	1704	6	BD082847 Human tum
34	547.6	92.7	1704	9	HSU81232 Human tum
35	477.2	80.7	852	9	AF147720 Chloroceb
36	340.2	57.6	976	6	AR270374 Sequence
37	309.6	52.4	477	6	AX892677 Sequence
38	309.6	52.4	477	6	BD028210 Sequence
39	304.6	51.5	2692	6	BD260132 Human tum
40	304.6	51.5	2692	6	AX022026 Sequence
41	261.2	44.2	858	10	AF515707 Mus muscu
42	261.2	44.2	893	10	AY266405 Mus muscu
43	259.6	43.9	1082	6	AX816349 Sequence
44	252.4	42.7	2604	9	AK124010 Homo sapi
45	250.8	42.4	1756	9	BC029848 Homo sapi

ALIGNMENTS

RESULT 1
AR168183
LOCUS AR168183
DEFINITION Sequence 19 from patent US 6287808.
ACCESSION AR168183
VERSION AR168183.1 GI:17904009
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 591)
AUTHORS Busfield,S.J.
TITLE Molecules of the herpesvirus-entry-mediator-related protein family
and uses thereof
JOURNAL Patent: US 6287808-A 19 11-SEP-2001;
linear DNA 591 bp PAT 17-DEC-2001

PR	03-SEP-1998 US	09/146950, 29-JUN-1999 US	09/342767 PI
SAMANHA J BUSFIELD			
PC	C12N15/09,A61K48/00,A61P19/02,A61P29/00,A61P31/10,A61P31/12,A61P35/00,A61P37/02,A61P37/08,C07K14/715,C07K16/28,C12N5/10,C12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/566/(C12P21/02,C12R1/91),C12N15/00,C12N5/00		
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CC	protein family		
CC	Location/Qualifiers		
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CC	/mol_type="genomic DNA"		
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CC	Best Local Similarity 100.0%; Pred. No. 5.8e-114;		
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CC	181 TATCGTGAAGAGGACCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTGCCTTCCA 240		
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CC	DEFINITION	PAT 17-DEC-2001	
CC	ACCESSION	AR168182	
CC	VERSION	AR168182.1	GI:17904008
CC	KEYWORDS		

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LOCUS AR169917 4622 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 6 from patent US 6291207.
ACCESSION AR169917
VERSION AR169917.1 GI:17907876
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4622)
AUTHORS Spear, P.G. and Montgomery, R.I.
TITLE Herpes virus entry receptor protein
JOURNAL Patent: US 6291207-A 6 18-SEP-2001;
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Location/Qualifiers
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Matches 558; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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RESULT 6
LOCUS AR172621 4622 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 6 from patent US 630336.
ACCESSION AR172621
VERSION AR172621.1 GI:17912112
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4622)
AUTHORS Spear, P.G. and Montgomery, R.I.
TITLE Antibody to Herpes virus entry receptor protein
JOURNAL Patent: US 630336-A 6 03-JUN-2003;
FEATURES
Location/Qualifiers

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4622)
AUTHORS Spear, P.G. and Montgomery, R.I.
TITLE Herpes virus entry receptor protein
JOURNAL Patent: US 630336-A 6 16-OCT-2001;
FEATURES
Location/Qualifiers
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Query Match 93.5%; Score 552.6; DB 6; Length 4622;
Best Local Similarity 98.4%; Pred. No. 4.6e-106;
Matches 558; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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121 TCCTGCAAGAGGAGCAGTACCCAGTGGGCTCCGAGTGTCTGCCCAAGTCAGTCCAGGT 180
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604 CACCAGACCAATTTGGCCTTAATCATATG 630

RESULT 7
LOCUS AR340583 4622 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 6 from patent US 6573058.
ACCESSION AR340583
VERSION AR340583.1 GI:33732243
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4622)
AUTHORS Spear, P.G. and Montgomery, R.I.
TITLE Antibody to Herpes virus entry receptor protein
JOURNAL Patent: US 6573058-A 6 03-JUN-2003;
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Location/Qualifiers

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Query Match          93.5%; Score 552.6; DB 6; Length 4622;
Best Local Similarity 98.4%; Pred. No. 4.6e-106;
Matches 558; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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SULT 8
244703
TUS
FINITION
Novel molecules of the herpesvirus-entry-mediator-related protein
family and uses thereof.
BD244703
BD244703
BD244703.1 GI:33054473
WORDS
JP 2002529051-A/23.
JCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
(bases 1 to 831)
Busfield,S.J.
Novel molecules of the herpesvirus-entry-mediator-related protein
family and uses thereof
Patent: JP 2002529051-A 23 10-SEP-2002;
MILLENNIUM PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002529051-A/23
PD 10-SEP-2002
PF 03-SEP-1999 JP 2000568973
PR 03-SEP-1998 US 09/146950,29-JUN-1999 US 09/342767 PI
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SAVANTHA J BUSFIELD
PC C12N15/09,A61K48/00,A61P19/02,A61P29/00,A61P31/10,A61P31/12,
PC A61P35/00,
PC A61P37/02,A61P37/08,C07K14/715,C07K16/28,C12N5/10,C12P21/02,
PC C12Q1/02,
PC C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/566//C12P21/02,
PC C12R1/91,
PC C12N15/00,C12N5/00
CC Novel molecules of the herpesvirus-entry-mediator-related CC
protein family
CC and uses thereof Location/Qualifiers
FH Key (1)..(831).
FT CDS
FEATURES             source
Query Match          93.2%; Score 550.8; DB 6; Length 831;
Best Local Similarity 99.6%; Pred. No. 1.5e-105;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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LOCUS
DEFINITION
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TNFRSF14-V241I allele, complete cds.
ACCESSION
AF373878
VERSION
AF373878.1 GI:17901872
KEYWORDS
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URCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 852)
 AUTHORS Struyf, F., Posavad, C.M., Keyaerts, E., Van Ranst, M., Corey, L. and
 Spear, P.G.
 TITLE Search for Polymorphisms in the Genes for Herpesvirus Entry
 Mediator, Nectin-1, and Nectin-2 in Immune Seronegative Individuals
 J. Infect. Dis. 185 (1), 36-44 (2002)
 JOURNAL 11756979
 PUBLISHED 2 (bases 1 to 852)
 REFERENCE Struyf, F., Posavad, C.M., Keyaerts, E., Van Ranst, M., Corey, L. and
 Spear, P.G.
 TITLE Direct Submission
 Submitted (24-APR-2001) Microbiology-Immunology, Northwestern
 University Medical School, 320 E. Superior, Searle 6-447, Chicago,
 IL 60611, USA
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 Best Local Similarity 99.6%; Pred. No. 1.5e-105;
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 DEFINITION HVEM polypeptides and uses thereof.
 ACCESSION BD091696
 VERSION BD091696.1 GI:22637307
 KEYWORDS JP 2001526632-A/1.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 927)
 AUTHORS Ashkenazi, A.J. and Marsters, S.A.
 TITLE HVEM polypeptides and uses thereof
 JOURNAL Patent: JP 2001526632-A 1 18-DEC-2001;
 GENENTECH INC
 COMMENT PN JP 2001526632-A/1
 PD 18-DEC-2001
 PP 05-DEC-1997 JP 1998526821
 PR 12-DEC-1996 US 60/032705
 PI AVI J ASHKENAZI, SCOT A MARSTERS
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 Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Fahey, J., Helton, E., Ketterman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalilus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 On Aug 19, 2003 this sequence version replaced gi:12803894.
 Contact: MGC help desk
 Email: cgapbs-re@mail.nih.gov
 Tissue Procurement: ATCC/DCTP/DTF
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@hgrl.nih.gov
 Akhter, N., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Mastriani, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgueon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 12 Row: P Column: 3
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23200040.

FEATURES

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1. 1612

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1. 1612

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member 14, precursor"

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LQNCPPGTFSPGLEEQHQTCKSLWTKAGATCTSSHWVFLGSLVIVIVCSF

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TGRSPNH"

390..683

misc_feature

ORIGIN

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 Best Local Similarity 99.6%; Pred. No. 1.3e-105;
 Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 DB 267 ATGAGCCCTCTCGAGACTGGGGGCTCTCTCCCTCGAGATCCACCCCGAGACCGACGTC 326

QY 61 TTGAGGCTGGTGTATCTACACCTTTCTGGAGAGCCCTCTGTACGCCCCAGCTCTGCGG 120
 DB 327 TTGAGGCTGGTGTATCTACACCTTTCTGGAGAGCCCTCTGTACGCCCCAGCTCTGCGG 386

QY 121 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCAGTGTCTGCCCGCCAGTGCAGTCCAGT 180
 DB 387 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCAGTGTCTGCCCGCCAGTGCAGTCCAGT 446

QY 181 TATCTGTGAAGAGGAGGCTCGGGGAGCTCACGGGACACAGTGTGTGAACCCCTGCCCTCCA 240
 DB 447 TATCTGTGAAGAGGAGGCTCGGGGAGCTCACGGGACACAGTGTGTGAACCCCTGCCCTCCA 506

QY 241 GGCACCTACATTGCGGACCTCAATGCTTAAGCAAGTGTCTGCAAGTGCACAAATGTGTGAC 300
 DB 507 GGCACCTACATTGCGGACCTCAATGCTTAAGCAAGTGTCTGCAAGTGCACAAATGTGTGAC 566

QY 301 CCAGCCATGGGCTCGCGGAGCGGAACTGTCTCAGGACACAGAACCCCTGTGTGTGTC 360
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QY 361 TGCAGCCAGGACCACTTCTCATCTGTCAGGACGAGGACCACTGCGCCGCGCGCGCT 420
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 DB 807 CACCAGACCAATTG 820

RESULT 13

AR169913

LOCUS

Sequence 1 from patent US 6291207.

DEFINITION

AR169913

ACCESSION

VERSION

AR169913.1

GI:17907872

KEYWORDS

Unknown.

SOURCE

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 1724)

AUTHORS

Spear, P.G. and Montgomery, R.I.

TITLE

Herpes virus entry receptor protein

JOURNAL

Patent: US 6291207-A 1 18-SEP-2001;

FEATURES

Location/Qualifiers

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 354 TTGAGGCTGGTGTATCTACCTTCTGGAGAGCCCTGTAGAGATCCACCCAGAACCGAGCTC 413
 121 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTGTCGCCCAAGTGCAGTCCAGGT 180
 414 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTGTCGCCCAAGTGCAGTCCAGGT 473
 191 TATCGTGTGAGGAGGCTTCGCGGAGCTGACGGGACAGTGTGTCGCCCAAGTGCAGTCCAGGT 240
 474 TATCGTGTGAGGAGGCTTCGCGGAGCTGACGGGACAGTGTGTCGCCCAAGTGCAGTCCAGGT 533
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 654 TGCAGCCAGGCTCTCTCTCTGATCGTCCAGGAGGGGACCACTGCGCGCGCTGCGCGCT 713
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RESULT 14
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 DEFINITION Sequence 1 from patent US 6303336.
 ACCESSION ARI72617
 VERSION ARI72617.1 GI:17912108
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1724)
 AUTHORS Spear, P.G. and Montgomery, R.I.
 TITLE Herpes virus entry receptor protein
 JOURNAL Patent: US 6303336-A 1 16-OCT-2001;
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IGIN

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1 ATGAGAGCTCTGAGAGCTGGGGGCTCTCTCTCTGAGATCCACCCAGAACCGAGCTC 60
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QY 121 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCAGTGTGTCGCCCAAGTGCAGTCCAGGT 180
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 QY 541 CACGAGACCAATTG 554
 DB 834 CACGAGACCAATTG 847

RESULT 15
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 LOCUS Novel molecules of the herpesvirus-entry mediator-related protein
 DEFINITION family and uses thereof.
 ACCESSION BD244687
 VERSION BD244687.1 GI:33054457
 KEYWORDS JP 2002529051-A/7.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1724)
 AUTHORS Busfield, S.J.
 TITLE Novel molecules of the herpesvirus-entry mediator-related protein
 JOURNAL Patent: JP 2002529051-A 7 10-SEP-2002;
 COMMENT MILLENNIUM PHARMACEUTICALS INC
 OS Homo sapiens (human)
 PN JP 2002529051-A/7
 PD 10-SEP-2002
 PF 03-SEP-1999 JP 2000568973
 PR 03-SEP-1998 US 09/146950, 29-JUN-1999 US 09/342767 PI
 SAMANTHA J BUSFIELD
 PC C12N15/00, A61K48/00, A61P19/02, A61P29/00, A61P31/10, A61P31/12,
 PC A61P35/00,
 PC A61P37/02, A61P37/08, C07K14/715, C07K16/28, C12N5/10, C12P21/02,
 PC C12Q1/02,
 PC C12Q1/68, G01N33/15, G01N33/50, G01N33/53, G01N33/566, (C12P21/02,
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 PC C12R1/91),
 CC Novel molecules of the herpesvirus-entry mediator-related CC
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 FH Key Location/Qualifiers
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Query Match      93.2%; Score 550.8; DB 6; Length 1724;
Best Local Similarity 99.6%; Pred. No. 1.3e-105;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGGAGCCTCTGAGAGCTGGGGCCCTCTCCCTGGAGATCCACCCCGCAGAACCGACGTC 60
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294 ATGGAGCCTCTGAGAGCTGGGGCCCTCTCCCTGGAGATCCACCCCGCAGAACCGACGTC 353
|||||
61 TTGAGGCTGGTGTATCTATCTCACTTTCTGGAGCCCCCTGTACGCCCCAGCTCTGCCG 120
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354 TTGAGGCTGGTGTATCTATCTCACTTTCTGGAGCCCCCTGTACGCCCCAGCTCTGCCG 413
|||||
121 TCCTCAGAGGAGGACAGTACCCAGTGGGCTCCAGTGTCTGCCCCAAAGTCAGTCCAGGT 180
|||||
414 TCCTCAGAGGAGGACAGTACCCAGTGGGCTCCAGTGTCTGCCCCAAAGTCAGTCCAGGT 473
|||||
181 TATCGTGTGAAGGAGGCTGCGGGAGCTGACGGGCACAGTGTGTGAACCCCTGCCCTCCA 240
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DB time : 2484 secs

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10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	591	100.0	1596	3	AAZ94197	Aaz94197 Soluble h
3	591	100.0	1596	7	ABX90565	Abx90565 Human CDN
4	550.8	93.2	831	7	ABX90578	Abx90578 Human mem
5	550.8	93.2	927	2	AAV44852	Aav44852 Herpesvir
6	550.8	93.2	927	2	AAV44852	Aav44852 CDNA clon
7	550.8	93.2	1049	3	AAZ49727	Aaz49727 Human PRO
8	550.8	93.2	1049	3	AAZ46931	Aaz46931 CDNA enco
9	550.8	93.2	1724	6	ABK94410	Abk94410 Human CDN
10	550.8	93.2	1724	7	ABX90562	Abx90562 Human mem
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12	550.8	93.2	1724	7	ABZ99577	Abz99577 Human cob
13	550.8	93.2	1724	8	ADA43034	Ada43034 Human her
14	550.8	93.2	1834	3	AAZ94198	Aaz94198 Membrane-
15	550.8	93.2	1834	7	ABX90577	Abx90577 Human mem
16	550	93.1	579	7	ABX90557	Abx90557 Human ORF
17	550	93.1	1815	4	AAZ03021	Aaz03021 Human dia
18	550	93.1	1929	3	AAZ94195	Aaz94195 Soluble h
19	550	93.1	1929	7	ABX90556	Abx90556 Human CDN
20	549.2	92.9	881	2	AAT40048	Aat40048 Human tum
21	549.2	92.9	881	3	AAZ28149	Aaz28149 Human TR2
22	549.2	92.9	1704	3	AAZ28135	Aaz28135 Human TR2
23	548.4	92.8	558	7	ABX90572	Abx90572 Human ORF

24	548.4	92.8	2313	3	AAZ94197	Aaz94197 Soluble h
25	548.4	92.8	2313	7	ABX90571	Abx90571 Human CDN
26	547.6	92.7	1704	2	AAV34509	Aav34509 Human TNF
27	547.6	92.7	1704	2	AAV83763	Aav83763 Human tum
28	544.4	92.1	1724	2	AAT51737	Aat51737 Human her
29	544.4	92.1	1724	2	AAZ25512	Aaz25512 Herpes vi
30	340.2	57.6	976	7	ACA56339	Aca56339 Human sig
31	309.6	52.4	477	3	AAC04465	Aac04465 Human sec
32	304.6	51.5	723	2	AAT40049	Aat40049 Human tum
33	304.6	51.5	2692	2	AAV34510	Aav34510 Human TNF
34	304.6	51.5	2692	2	AAZ28147	Aaz28147 Human TR2
35	239.4	40.5	2637	2	AAV34511	Aav34511 Human TNF
36	239.4	40.5	2637	2	AAZ28148	Aaz28148 Human TR2
37	233.8	39.6	447	8	ACH16324	Ach16324 Human adu
38	233.4	39.5	405	2	AAT40050	Aat40050 Human tum
39	162.2	27.4	9159	4	AAK83488	Aak83488 Human imm
40	126	21.3	126	7	ABX90575	Abx90575 Human sol
41	126	21.3	126	7	ABX90576	Abx90576 Human sol
42	126	21.3	126	7	ABX90561	Abx90561 Human sol
43	126	21.3	126	7	ABX90560	Abx90560 Human sol
44	126	21.3	126	7	ABX90569	Abx90569 Human sol
45	126	21.3	126	7	ABX90582	Abx90582 Human mem

ALIGNMENTS

RESULT 1
ABX90566
ID ABX90566 standard; cDNA; 591 BP.
XX
AC ABX90566;
XX
DT 06-MAY-2003 (first entry)
XX
DE Human ORF for soluble Herpesvirus Entry Mediator-2 (SHVEM-2).
XX
KW Human; ss: gene: TANGO-69 receptor; herpesvirus entry mediator; HVEM;
KW SHVEM1; SHVEM2; SHVEM3; mHVEM2; tumour necrosis factor receptor; TNFR;
KW immune disorder; autoimmune disorder; arthritis; graft rejection;
KW T-cell disorder; AIDS; inflammatory disorder; bacterial infection;
KW psoriasis; septicemia; cerebral malaria; inflammatory bowel disease;
KW rheumatoid arthritis; osteoarthritis; allergic inflammatory disorder;
KW asthma; psoriasis; apoptotic disorder; rheumatoid arthritis;
KW systemic lupus erythematosus; insulin-dependent diabetes mellitus;
KW cytotoxic disorder; septic shock; cachexia; proliferative disorder;
KW B-cell cancer.
XX
OS Homo sapiens.
XX
PN US2002132297-A1.
XX
PD 19-SEP-2002.
XX
PF 21-AUG-2001; 2001US-00934289.
XX
PR 03-SEP-1998; 98US-00146950.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Busfield SJ;
XX
DR WPI; 2003-255106/25.
XX
DR P-PSDB; ABU60682.
XX
PT New TANGO-69 receptor polynucleotides and polypeptides, useful for
PT treating arthritis, graft rejection, AIDS, bacterial infection,
PT psoriasis, septicemia, cerebral malaria, inflammatory bowel disease,
PT asthma, psoriasis, lupus.
XX
PS Claim 2; Fig 3; 79pp; English.
XX
PS The invention relates to an isolated nucleic acid molecule, designated as

/*tag= a
/product= "HVEM"

WO9825967-A1.

18-JUN-1998.

05-DEC-1997; 97WO-US022278.

12-DEC-1996; 96US-0032705P.

(GETH) GENENTECH INC.

Ashkenazi AJ, Marsters SA;

WPI; 1998-348457/30.

P-PSDB; AAW69238.

Herpesvirus entry mediator polypeptide, HVEM - useful, e.g. in assays for HVEM and to produce antibodies and transgenic animals, e.g. for drug screening.

Example 1; Fig 1; 46pp; English.

This sequence encodes the herpesvirus entry mediator (HVEM) protein of the invention. The protein is useful in quantitative diagnostic assays for HVEM, in affinity purification of HVEM from recombinant cells/natural sources and in competitive-type receptor binding assays. It can also be used to generate antibodies, also useful in diagnostic assays for HVEM and affinity purification of HVEM. HVEM is believed to be a member of the tumour necrosis factor receptor (TNFR) family, and transient transfection of HVEM into human 293 cells caused marked activation of certain transcription factors, e.g. AP-1, suggesting that HVEM is involved in regulating gene expression in response to infectious stimuli and cellular stress. The predominant expression of HVEM mRNA in lymphocyte-rich tissues (e.g. spleen and peripheral blood) also suggested it may be a receptor in regulating lymphocyte activity. Antibodies produced may therefore be useful therapeutically, e.g. antagonistic antibodies may be useful to block excessive inflammatory/autoimmune response resulting from e.g. AP-1 induction, whilst agonistic antibodies may enhance HVEM regulation of such induction. The DNA may be used diagnostically, e.g. to determine if DNA and/or RNA encoding HVEM is present in cells, and to prepare HVEM polypeptide recombinantly. It is also useful to produce non-human transgenic animals (e.g. mice or rats), especially knockout animals containing cells with an altered gene encoding HVEM polypeptide. Such animals are useful in the development and screening of therapeutically useful reagents. (Updated on 17-OCT-2003 to standardise OS field)

Sequence 927 BP; 185 A; 286 C; 291 G; 165 T; 0 U; 0 Other;

Query Match 93.2%; Score 550.8; DB 2; Length 927;
Best Local Similarity 99.6%; Pred. No. 1e-129;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1 ATGGAGCTCTGGAGCTGGGGGCTCTCTCTGGAGATCCACCCCGAACCGAGTC 60
76 ATGGAGCTCTGGAGCTGGGGGCTCTCTCTGGAGATCCACCCCGAACCGAGTC 135
61 TTGAGGCTGTGTCTATCTACCTTTCTGGAGCCCTCTACGCCCCAGCTCTGCCG 120
136 TTGAGGCTGTGTCTATCTACCTTTCTGGAGCCCTCTACGCCCCAGCTCTGCCG 195
121 TCCTCAAGGAGGACGATACCAAGTGCGCTCCAGTGCTGCCCAAGTCAGTCAGGT 180
196 TCCTCAAGGAGGACGATACCAAGTGCGCTCCAGTGCTGCCCAAGTCAGTCAGGT 255
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256 TATCTGTGTAGGAGGCTCGGGGAGCTGACGGGACAGTGCTGAACTCCCTCCCA 315
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316 GGCACCTACATTGCCACCTCAATGGCCCTAAGCAAGTGCTTGCAAGTCCCAATGTGAC 375

QY 301 CCAGCCATGGGCTGCGCGAGCCGGAATCTGCTCCAGGACAGAGAACCCGCTGTGTGC 360
DB 376 CCAGCCATGGGCTGCGCGAGCCGGAATCTGCTCCAGGACAGAGAACCCGCTGTGTGC 435
QY 361 TGCAGCCAGGCACTTCTGCATGCTCAGGACGGGACCACTGCGCCCGCTGCCCGCT 420
DB 436 TGCAGCCAGGCACTTCTGCATGCTCAGGACGGGACCACTGCGCCCGCTGCCCGCT 495
QY 421 TAGCCACCTCCAGCCCGGGCCAGAGGTCGAGAGGAGGACCCAGAGAGTCAGGACACC 480
DB 496 TAGCCACCTCCAGCCCGGGCCAGAGGTCGAGAGGAGGACCCAGAGAGTCAGGACACC 555
QY 481 CTGTGTCAGAACTGCCCGCCCGGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTGAC 540
DB 556 CTGTGTCAGAACTGCCCGCCCGGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTGAC 615
QY 541 CACCAGACCAATTG 554
DB 616 CACCAGACCAATTG 629

RESULT 6

AAX87265
ID AAX87265 standard; cDNA; 927 BP.

AC AAX87265;

DT 27-SEP-1999 (first entry)

DE cDNA clone encoding human PRO509, amplified in tumour cells.

KW PRO509; UNQ329; tumour necrosis factor receptor; cancer; diagnosis;
KW therapy; human; HVEM; ss.

OS Homo sapiens.

FH Key Location/Qualifiers
FT CDS 76..927
FT /*tag= a

XX WO9935170-A2.

XX 15-JUL-1999.

XX 05-JAN-1999; 99WO-US000106.

XX 05-JAN-1998; 98US-0070440P.

XX 29-APR-1998; 98US-0083500P.

XX 22-MAY-1998; 98US-0086414P.

XX 10-JUN-1998; 98US-0088742P.

XX 10-NOV-1998; 98US-0107783P.

XX 20-NOV-1998; 98US-0109304P.

XX (GETH) GENENTECH INC.

XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA, Roy MA;

XX Wood WI;

XX WPI; 1999-430385/36.

XX P-PSDB; AAY06488.

XX Antibody against proteins expressed in neoplastic cells, useful for tumor diagnosis and treatment.

XX Example 1; Fig 23; 162pp; English.

XX This is the nucleotide sequence of cDNA clone DNA50148 (HVEM) coding for human PRO509 (UNQ329) (see AAY06488), a member of the tumour necrosis factor receptor family. Amplification of DNA50148 occurs in various CC tumours, suggesting an association with tumour formation or growth. CC Antagonists (e.g. antibodies) directed to PRO509 may have use in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are

C amplified in the genome of tumour cells. Such amplification is expected
C to be associated with overexpression of the gene product and to
C contribute to tumorigenesis. The encoded proteins (see AA06477-90) may
C be useful targets for the diagnosis and/or treatment (including
C prevention) of certain cancers, and may act as predictors of the
C prognosis of tumour treatment
X
Q Sequence 927 BP; 185 A; 286 C; 291 G; 165 T; 0 U; 0 Other;

Query Match 93.2%; Score 550.8; DB 2; Length 927;
Best Local Similarity 99.6%; Pred. No. 1e-129;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Y 1 ATGAGCCTCTGGAGACTGGGGGCTCTCCCTGGAGATCCACCCCGAGACCGACGTC 60
b 76 ATGAGCCTCTGGAGACTGGGGGCTCTCCCTGGAGATCCACCCCGAGACCGACGTC 135
Y 61 TTGAGGCTGTGTGTATCTCACTTTCTGGAGGCCCCCTGTACGCCCGACGCTTGCG 120
b 136 TTGAGGCTGTGTGTATCTCACTTTCTGGAGGCCCCCTGTACGCCCGACGCTTGCG 195
Y 121 TCCTGCAAGGAGACGAGTACCCAGTGGGCTCGAGTGTGCTGCCCAAGTCAGTCCAGGT 180
b 196 TCCTGCAAGGAGACGAGTACCCAGTGGGCTCGAGTGTGCTGCCCAAGTCAGTCCAGGT 255
Y 181 TATCGTGTGAAGAGGCTCTGGGGAGCTGACGGGCACAGTGTGTGAACCTTGCCCTCCA 240
b 256 TATCGTGTGAAGAGGCTCTGGGGAGCTGACGGGCACAGTGTGTGAACCTTGCCCTCCA 315
Y 241 GGCACTTACATTTGCCACCTCAATGGCCTTAAGCAAGTGTCTCAGTGCATATGTGTGAC 300
b 316 GGCACTTACATTTGCCACCTCAATGGCCTTAAGCAAGTGTCTCAGTGCATATGTGTGAC 375
Y 301 CCAGCCATGGGCTGTGGCGGAGCCGGAAGTGTCTCCAGGACAGAGAACGCGTGTGTGGC 360
b 376 CCAGCCATGGGCTGTGGCGGAGCCGGAAGTGTCTCCAGGACAGAGAACGCGTGTGTGGC 435
Y 361 TGCAGCCAGGCGCACTTCTCATCTGTCAGGAGCGGACCACTGCGCGCGCTGCGCGCT 420
b 436 TGCAGCCAGGCGCACTTCTCATCTGTCAGGAGCGGACCACTGCGCGCGCTGCGCGCT 495
Y 421 TACGCCACTTCCAGCCGCGGAGGGGTGCAGAGGGAGGACCGAGAGTCAGACACACC 480
b 496 TACGCCACTTCCAGCCGCGGAGGGGTGCAGAGGGAGGACCGAGAGTCAGACACACC 555
Y 481 CTGTGTGAGAACTGCCCCCGGGGACCTTCTTCCCAATGGGACCTTGGAGGAATGTGAG 540
b 556 CTGTGTGAGAACTGCCCCCGGGGACCTTCTTCCCAATGGGACCTTGGAGGAATGTGAG 615
Y 541 CACCAGACCAATTG 554
b 616 CACCAGACCAATTG 629

RESULT 7
AA49727
D AA49727 standard; cdna; 1049 BP.
C
C AAA49727;
T 25-SEP-2000 (first entry)
E Human PRO509 cDNA clone DNA50148-1068.
X PRO509; human; antitumour; tumour; therapy; cytostatic; breast cancer;
W ovarian cancer; renal cancer; colorectal cancer; uterine cancer;
W prostate cancer; lung cancer; bladder cancer;
W central nervous system cancer; melanoma; leukaemia; neoplasm; ss.
X Homo sapiens.
X Key Location/Qualifiers
H CDS 82..933

FT sig_peptide /*tag= a
FT mat_peptide /*tag= b
FT /*tag= c
XX WO200037638-A2.
XX 29-JUN-2000.
XX 02-DEC-1999; 99WO-US028565.
XX 22-DEC-1998; 98US-0113296P.
PR 08-MAR-1999; 99WO-US005028.
PR 21-APR-1998; 98US-0130232P.
PR 28-APR-1999; 99US-013445P.
PR 14-MAY-1999; 99US-0134287P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
XX (GETH) GENENTECH INC.
PA Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Marsters SA;
XX Napier MA, Pitti RM, Wood WI;
PI WPI; 2000-442668/38.
XX P-PSDB; AAY95348.
DR Novel composition to inhibit neoplastic cell growth or for treating tumor
XX in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO219, PRO221,
XX PRO224, PRO328, PRO301, PRO526, PRO356, PRO509 or PRO866.
XX Claim 20; Fig 23; 172pp; English.
XX The present sequence is that of cDNA clone DNA50148-1068 encoding human
XX PRO509 (see AA195348), a novel antitumour protein that shows homology to
XX the tumour necrosis factor receptor family. The cDNA was isolated from a
XX human retina cDNA library by hybridisation. A claimed method for
XX inhibiting the growth of a tumour cell comprises exposing the tumor cell
XX to PRO179, PRO207, PRO320, PRO219, PRO224, PRO328, PRO301,
XX PRO526, PRO362, PRO356, PRO509 or PRO866 (see AAY95337-49), their
XX agonists or chimeric polypeptides incorporating them. The tumour is
XX especially a cancer selected from breast, ovarian, renal, colorectal,
XX uterine, prostate, lung, bladder and central nervous system cancer,
XX melanoma and leukaemia. Nucleic acids encoding PRO179 etc. are used in
XX the recombinant production of the antitumour polypeptides
SQ Sequence 1049 BP; 208 A; 330 C; 332 G; 179 T; 0 U; 0 Other;

Query Match 93.2%; Score 550.8; DB 3; Length 1049;
Best Local Similarity 99.6%; Pred. No. 1.1e-129;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAGCCTCTGGAGACTGGGGGCTCTCCCTGGAGATCCACCCCGAGACCGACGTC 60
DB 82 ATGAGCCTCTGGAGACTGGGGGCTCTCCCTGGAGATCCACCCCGAGACCGACGTC 141
QY 61 TTGAGGCTGTGTGTATCTCACTTTCTGGAGGCCCCCTGTACGCCCGACGCTTGCG 120
DB 142 TTGAGGCTGTGTGTATCTCACTTTCTGGAGGCCCCCTGTACGCCCGACGCTTGCG 201
QY 121 TCCTGCAAGGAGACGAGTACCCAGTGGGCTCCGAGTGTGCTGCCCAAGTCAGTCCAGGT 180
DB 202 TCCTGCAAGGAGACGAGTACCCAGTGGGCTCCGAGTGTGCTGCCCAAGTCAGTCCAGGT 261
QY 181 TATCGTGTGAAGAGGCTCTGGGGAGCTGACGGGACAGTGTGTGAACCTTGCCCTCCA 240
DB 262 TATCGTGTGAAGAGGCTCTGGGGAGCTGACGGGACAGTGTGTGAACCTTGCCCTCCA 321
QY 241 GGCACTTACATTTGCCACCTCAATGGCTTAAGCAAGTGTCTCAGTGCATATGTGTGAC 300

322 GGCACTTACATTGCCACCTCAATGCGCTAAGCAAGTGTCTGAGTGCACCAATGTGTGAC 381
301 CCAGCCATGGCTGGCGCGAGCCGGAATCTCTCAGACAGAGAACCCGTGTGTGGC 360
382 CCAGCCATGGCTGGCGCGAGCCGGAATCTCTCAGACAGAGAACCCGTGTGTGGC 441
361 TGCAGCCAGGCGCACTTCTCATGCTCCAGGACGGGACCACTGTGGCCGCGTGC 420
442 TGCAGCCAGGCGCACTTCTCATGCTCCAGGACGGGACCACTGTGGCCGCGTGC 501
421 TACGCCACCTCCAGCCCGGCCAGAGGGGTGCAGAGGGAGGCACCGAGAGTCAGACACC 480
502 TACGCCACCTCCAGCCCGGCCAGAGGGGTGCAGAGGGAGGCACCGAGAGTCAGACACC 561
481 CTGTGTGAGAACTGCCCGCCCGGGACCTTCTCTCCCAATGGGACCCCTGAGGAATGTGAC 540
562 CTGTGTGAGAACTGCCCGCCCGGGACCTTCTCTCCCAATGGGACCCCTGAGGAATGTGAC 621
541 CACCAGACCAATTG 554
622 CACCAGACCAAGTG 635

SULT 8
A46931

AAA46931 standard; cDNA; 1049 BP.

AAA46931;

03-OCT-2000 (first entry)

cDNA encoding novel polypeptide PRO509.

PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715;
PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell; tumourigenesis;
cancer; neoplastic cell growth; cell proliferation; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 82..933
/*tag= a

WO200037640-A2.

29-JUN-2000.

16-DEC-1999; 99WO-US030095.

22-DEC-1998; 98US-0113296P.

08-MAR-1999; 99WO-US005028.

02-JUN-1999; 99WO-US012252.

01-SEP-1999; 99WO-US020111.

15-SEP-1999; 99WO-US021090.

30-NOV-1999; 99WO-US028313.

30-NOV-1999; 99WO-US028409.

01-DEC-1999; 99WO-US028301.

02-DEC-1999; 99WO-US028565.

(GETH) GENENTECH INC.

Borstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;
Wood WI;

WPI; 2000-452188/39.

P-PSDB; AAY93695.

New anti-polypeptide antibody useful in the treatment and diagnosis of
neoplastic cell growth and proliferation.

Claim 50; Fig 23; 220pp; English.

The present sequence encodes a novel human polypeptide. The specification

CC describes novel polypeptides designated PRO201, PRO292, PRO327, PRO1265,
CC PRO344, PRO343, PRO347, PRO357, PRO715, PRO1017, PRO1112, PRO509, PRO853
CC and PRO882. These genes are amplified in the genome of tumour cells. The
CC polypeptides are believed to contribute to tumourigenesis. The
CC polypeptides are useful target for the identification of certain cancers,
CC and may act as predictors of the prognosis of tumour treatment.
CC Antibodies against these polypeptides are useful in the treatment and
CC diagnosis of neoplastic cell growth and proliferation in mammals
XX
SQ Sequence 1049 BP; 208 A; 330 C; 332 G; 179 T; 0 U; 0 Other;

Query Match 93.2%; Score 550.8; DB 3; Length 1049;
Best Local Similarity 99.6%; Pred. No. 1.1e-129;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAGCCCTCTCGAGACTGGGGCCCTCTCCCTGAGATCCACCCCCAGAACCCGACGTC 60
DB 82 ATGAGCCCTCTCGAGACTGGGGCCCTCTCCCTGAGATCCACCCCCAGAACCCGACGTC 141
QY 61 TTGAGGCTGTGTATCTTCTTCTGGAGCCCCCTGTACGCCCCAGCTCTGCGG 120
DB 142 TTGAGGCTGTGTATCTTCTTCTGGAGCCCCCTGTACGCCCCAGCTCTGCGG 201
QY 121 TCCTGCAAGAGACAGTACCCAGTGGGCTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 202 TCCTGCAAGAGACAGTACCCAGTGGGCTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 261
QY 181 TATCGTGTGAAGGAGGCGCTGCGGGAGCTGACGGGCACACAGTGTGTGAACCCCTGCCCTCCA 240
DB 262 TATCGTGTGAAGGAGGCGCTGCGGGAGCTGACGGGCACACAGTGTGTGAACCCCTGCCCTCCA 321
QY 241 GGCACCTTACATTCGCCCACTTAATGCGCTAAGCAAGTGTGCAAGTGTGCAAGTGTGCAAG 300
DB 322 GGCACCTTACATTCGCCCACTTAATGCGCTAAGCAAGTGTGCAAGTGTGCAAGTGTGCAAG 381
QY 301 CCAGCCATGGGCTGCGCGAGCGCGGAACTGCTCCAGACACAGAGAACCCCGTGTGTGGC 360
DB 382 CCAGCCATGGGCTGCGCGAGCGCGGAACTGCTCCAGACACAGAGAACCCCGTGTGTGGC 441
QY 361 TGCAGCCCGAGCCCACTTCTGCAATGCTCCAGAGAGGGACCACTGCGCCCGCTGCGCGCT 420
DB 442 TGCAGCCCGAGCCCACTTCTGCAATGCTCCAGAGAGGGACCACTGCGCCCGCTGCGCGCT 501
QY 421 TACGCCACCTCCAGCCCGGCCAGAGGGTGCAGAGGGAGGCACCGAGAGTCAGGACACC 480
DB 502 TACGCCACCTCCAGCCCGGCCAGAGGGTGCAGAGGGAGGCACCGAGAGTCAGGACACC 561
QY 481 CTGTGTGAGAACTGCCCGCCCGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTGAC 540
DB 562 CTGTGTGAGAACTGCCCGCCCGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTGAC 621
QY 541 CACCAGACCAATTG 554
DB 622 CACCAGACCAAGTG 635

RESULT 9

ABK84410

ID ABK84410 standard; cDNA; 1724 BP.

XX

AC ABK84410;

XX

DT 14-AUG-2002 (first entry)

XX

DE Human cDNA differentially expressed in granulocytic cells #981.

XX

KW Human; ss; granulocytic cell; DNA chip; bacterial infection;

KW viral infection; parasitic infection; protozoal infection;

KW fungal infection; sterile inflammatory disease; psoriasis;

KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;

KW cardiac reperfusion injury; renal reperfusion injury; ARDS;

KW adult respiratory distress syndrome; inflammatory bowel disease;

KW Crohn's disease; ulcerative colitis; periodontal disease;

granulocyte activation; chronic inflammation; allergy.

Homo sapiens.

WO200228999-A2.

11-APR-2002.

03-OCT-2001; 2001WO-US030821.

03-OCT-2000; 2000US-0237189P.

(GENE-) GENE LOGIC INC.

Beazer-Barclay Y, Weisman SM, Yamaga S, Vockley J;

WPI; 2002-435328/46.

Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.

Claim 1; SEQ ID NO 981; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) Gs by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences

Sequence 1724 BP; 331 A; 548 C; 512 G; 333 T; 0 U; 0 Other;

Query Match 93.2%; Score 550.8; DB 6; Length 1724;
Best Local Similarity 99.6%; Pred. No. 1.2e-129;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGAGGCTCTGAGACTGGGGCTCTCTCTGAGATCCACCCCGAGACCGTC 60

294 ATGAGGCTCTGAGACTGGGGCTCTCTCTGAGATCCACCCCGAGACCGTC 353

61 TTGAGGCTGGTGTATCTACCTTTCTGGAGCCCTCTGACCCCGAGCTTGGCG 120

354 TTGAGGCTGGTGTATCTACCTTTCTGGAGCCCTCTGACCCCGAGCTTGGCG 413

QY 121 TCCTGCAAGGAGGAGCTACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCAGTCCAGGT 180
DB 414 TCCTGCAAGGAGGAGCTACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCAGTCCAGGT 473
QY 181 TATCGTGTAAAGGAGGCTCGGGGAGCTGACGGGCAAGTGTGTGAACCTGCCCTCCA 240
DB 474 TATCGTGTAAAGGAGGCTCGGGGAGCTGACGGGCAAGTGTGTGAACCTGCCCTCCA 533
QY 241 GGCACCTACATTGCCCACTCAATGGGCTTAAGCAAGTGTGTGCAAGTCCCAATGTGTGAC 300
DB 534 GGCACCTACATTGCCCACTCAATGGGCTTAAGCAAGTGTGTGCAAGTCCCAATGTGTGAC 593
QY 301 CCAGCCATGGGCTCGGGCGAGCCGGAACCTGTCTCCAGGACAGAGACCGCGTGTGGC 360
DB 594 CCAGCCATGGGCTCGGGCGAGCCGGAACCTGTCTCCAGGACAGAGACCGCGTGTGGC 653
QY 361 TCGAGCCAGGCGCACTTCTGATGTCCAGGACGGGACCACTCGCGCGGCTGCGCGGCT 420
DB 654 TCGAGCCAGGCGCACTTCTGATGTCCAGGACGGGACCACTCGCGCGGCTGCGCGGCT 713
QY 421 TACGCCACCTCCAGCCCGGGCCAGAGGCTGAGAGGAGGACCGGAGAGTCAGGACACC 480
DB 714 TACGCCACCTCCAGCCCGGGCCAGAGGCTGAGAGGAGGACCGGAGAGTCAGGACACC 773
QY 481 CTGTGTCAAGTCCCGCGGGGACCTTCTCTCCATGGGACCTTCCAGTGGAGGAATGTGAC 540
DB 774 CTGTGTCAAGTCCCGCGGGGACCTTCTCTCCATGGGACCTTCCAGTGGAGGAATGTGAC 833
QY 541 CACCAGACCAATTG 554
DB 834 CACCAGACCAAGT 847
RESULT 10
ABX90562
ID ABX90562 standard; CDNA; 1724 BP.
XX
AC ABX90562;
XX
DT 06-MAY-2003 (first entry)
XX
DE Human membrane-bound Herpesvirus Entry Mediator (mHVM) CDNA.
XX
KW Human; ss; gene; TANGO-69 receptor; herpesvirus entry mediator; HVEM;
KW SHVEM1; SHVEM2; mHVM3; mHVM2; tumour necrosis factor receptor; TNFR;
KW immune disorder; autoimmune disorder; arthritis; graft rejection;
KW T-cell disorder; AIDS; inflammatory disorder; bacterial infection;
KW psoriasis; septicemia; cerebral malaria; inflammatory bowel disease;
KW rheumatoid arthritis; osteoarthritis; allergic inflammatory disorder;
KW asthma; psoriasis; apoptotic disorder; rheumatoid arthritis;
KW systemic lupus erythematosus; insulin-dependent diabetes mellitus;
KW cytotoxic disorder; septic shock; cachexia; proliferative disorder;
KW B-cell cancer.
XX
OS Homo sapiens.
XX
PN US2002132297-A1.
XX
PD 19-SEP-2002.
XX
PF 21-AUG-2001; 2001US-00934289.
XX
PR 03-SEP-1998; 98US-00146950.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Busfield SJ;
XX
DR WPI; 2003-255106/25.
DR P-PSDB; ABU60681.
XX
PT New TANGO-69 receptor polynucleotides and polypeptides, useful for

1 ATGGAGCCTCCTGGAGACTGGGGCCTCCTCCCTGGAGATCCACCCCGAACCGACGTC 60

2

541 CACCAGACCAATTG 554
|||||
834 CACCAGACCAAGTG 847

ULT 13
43034
ADA43034 standard; DNA; 1724 BP.

ADA43034;

20-NOV-2003 (first entry)

Human herpesvirus entry mediator (HVEM) gene for myeloma detection.

ds; gene; multiple myeloma; MGUS;
monoclonal gammopathy of undetermined significance;
plasma cell leukemia; WEE1; HVEM; human herpesvirus entry mediator;
histone H2A; LD78alpha; GIPR;
glucose-dependent insulinotropic polypeptide receptor; CTGF;
connective tissue growth factor; cytochrome b alpha-subunit;
major histocompatibility complex; MHC homologue;
thyroid hormone binding protein; THBP; cysteine-rich heart protein; CRHP;
liposome protein L28; growth factor receptor; immunoglobulin;
liposome receptor; liposome protein L18; NM23-H1; heat-shock protein;
laminin receptor; macrophage motility inhibitory factor;
K1AA1042 protein; APR peptide; RING6; human H-factor.

Human herpesvirus.

Key Location/Qualifiers
CDS 294..1145
/*tag= a
/product= "Human herpesvirus entry mediator protein"

WO2003038088-A1.

08-MAY-2003.

30-OCT-2002; 2002WO-JP011257.

02-NOV-2001; 2001JP-00337752.

(FUJI) FUJISAWA PHARM CO LTD.

Mano H;

WPI; 2003-430523/40.
P-PSDB; ADA43035.

Comparison of gene expression profile in tissue sample with known
profiles of normal and pathological tissue for determination of presence
and progression stage of multiple myeloma.

Disclosure; Page 79-82; 128pp; Japanese.

The invention relates to a method for the investigation of multiple
myeloma in which the expression level of genes associated with multiple
myeloma in a sample is compared with that in normal tissue or in MGUS
(monoclonal gammopathy of undetermined significance), MM (multiple
myeloma) or PCL (plasma cell leukaemia) stage multiple myeloma tissue.
The genes compared in the method include one or more of WEE1, HVEM,
histone H2A, LD78alpha, GIPR, CTGF, cytochrome b alpha-subunit, MHC
homologues, THBP, CRHP, liposome protein L28, growth factor receptor,
immunoglobulin Ig lambda-chain, laminin receptor, liposome protein L18,
NM23-H1, 28kDa heat-shock protein, immunoglobulin transcript 3 protein
variant 1, GsGR binding protein alpha-subunit, M9 macrophage motility
inhibitory factor, K1AA1042 protein, APR peptide, RING6, human H-factor
homologues and K1AA0832 protein genes. The method is useful for the
determination of the existence or stage of progression of multiple
myeloma and the risk of its development, and screening substances for
their ability to treat or prevent multiple myeloma. This sequence

CC represents the human herpesvirus entry mediator (HVEM) gene used in the
CC method of the invention.

XX Sequence 1724 BP; 331 A; 548 C; 512 G; 333 T; 0 U; 0 Other;

Query Match 93.2%; Score 550.8; DB 8; Length 1724;
Best Local Similarity 99.6%; Pred. No. 1.2e-129;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGAGCCTCTGGAGACTGGGGCTCTCCCTGGAGATCCACCCCGAGAACCGACGTC 60

Db 294 ATGGAGCCTCTCTGGAGACTGGGGCTCTCCCTGGAGATCCACCCCGAGAACCGACGTC 353

QY 61 TTGAGGCTGGTGTATCTCACCTTTCTGGAGCCCTCTGCTACGCCAGTCTGCGG 120

Db 354 TTGAGGCTGGTGTATCTCACCTTTCTGGAGCCCTCTGCTACGCCAGTCTGCGG 413

QY 121 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTGCCCCAAGTGCAGTCCAGGT 180

Db 414 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTGCCCCAAGTGCAGTCCAGGT 473

QY 181 TATCGTGTGAAGGAGGCTGCGGGAGCTGACGGGCACAGTGTGTGAACCTTCCCTCCA 240

Db 474 TATCGTGTGAAGGAGGCTGCGGGAGCTGACGGGCACAGTGTGTGAACCTTCCCTCCA 533

QY 241 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAGTCCCAATGTGTGAC 300

Db 534 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAGTCCCAATGTGTGAC 593

QY 301 CCAGCCATGGGCTGCGGGAGCGGGAATGTCTCCAGGACAGAGAACGCGTGTGTGGC 360

Db 594 CCAGCCATGGGCTGCGGGAGCGGGAATGTCTCCAGGACAGAGAACGCGTGTGTGGC 653

QY 361 TGCAGCCAGGCCCATTCTGTCATGTCAGGACGGGACCACTGCGCGGCTGCCGCGCT 420

Db 654 TGCAGCCAGGCCCATTCTGTCATGTCAGGACGGGACCACTGCGCGGCTGCCGCGCT 713

QY 421 TACGCCACTTCAGCCCGGCGCAGAGGTGCAGAGGGGACCGAGAGTFCAGGACACC 480

Db 714 TACGCCACTTCAGCCCGGCGCAGAGGTGCAGAGGGGACCGAGAGTFCAGGACACC 773

QY 481 CTGTGTCAAGACTGCCCCCGGGAGCCTTCTCTCCCAATGGGACCTTGGAGGAATGTCAG 540

Db 774 CTGTGTCAAGACTGCCCCCGGGAGCCTTCTCTCCCAATGGGACCTTGGAGGAATGTCAG 833

QY 541 CACCAGACCAATTG 554

Db 834 CACCAGACCAAGTG 847

RESULT 14

AAZ94198

ID AAZ94198 standard; cDNA; 1834 BP.

XX AAZ94198;

AC AAZ94198;

XX 19-JUN-2000 (first entry)

DT Membrane-bound herpesvirus entry mediator-2 (mHVEM2) cDNA.

DE mHVEM-2; membrane-bound herpesvirus entry mediator-2; TANGO-69-receptor;
tumour necrosis factor receptor; human; herpes simplex virus; infection;
cancer; inflammation; autoimmune disorder; therapy; diagnosis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT 103..936

FT CDS /*tag= a

FT 2" /*tag= "this coding region is separately claimed in Claim

FT sig_peptide 103..206

FT /*tag= b

mat_peptide 207..933
/*tag= C

W0200014230-A1.

16-MAR-2000.

03-SEP-1999; 99WO-US020180.

03-SEP-1998; 98US-00146950.

29-JUN-1999; 99US-00342767.

(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

Busfield SJ;

WPI; 2000-256981/22.

P-PSDB; AAY79207.

New nucleic acid molecule encoding herpes virus entry mediator (HVEM),
either in the soluble or membrane bound form, is useful in screening
assays and detection assays.

Claim 2; Fig 7; 149pp; English.

This full-length DNA sequence, the coding region of which is also
claimed, corresponds to cDNA encoding human membrane-bound herpesvirus
entry mediator-2 (mhVEM2, see AAY79207), a novel form of membrane-bound
herpesvirus entry mediator (mhVEM). mhVEM2 is a TANGO-69-receptor and
member of the tumour necrosis factor receptor (TNFR) superfamily. The
mhVEM2 cDNA, deposited as ATCC 207171, was identified in a human mixed
lymphocyte reaction library. HVEM mediates the entry of herpes simplex
virus (HSC) into cells. The invention is based on the discovery of 3 cDNA
molecules (see AAZ94195-97) which encode soluble forms (see AAY79204-06)
of mhVEM, and on the present cDNA encoding mhVEM2. In addition to
isolated full-length proteins and polynucleotides, and invention provides
TANGO-69-receptor fusion proteins, antigenic peptides and antibodies.
Also provided are recombinant expression vectors, host cells and
transgenic animals in which a TANGO-69-receptor gene has been introduced
or disrupted. DNA encoding HVEM, HVEM proteins and HVEM antibodies can be
used in screening and detection assays (e.g. chromosomal mapping, tissue
typing). HVEM proteins can also be used for regulation of cell
proliferation, cell differentiation, cell survival, inflammation mast
cell activity, HSV infection and/or proliferation, and/or coagulation.
HVEM agonists can be used to treat disorders associated with decreased
HVEM activity, e.g. proliferative disorders such as carcinoma or
pathogenic infection. Antagonists can be used to treat disorders
associated with increased HVEM activity, e.g. autoimmune, T cell,
inflammatory and allergic inflammation disorders

Sequence 1834 BP; 398 A; 556 C; 539 G; 341 T; 0 U; 0 Other;

Query Match 93.2%; Score 550.8; DB 3; Length 1834;
Best Local Similarity 99.6%; Pred. No. 1.2e-129;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
2Y 1 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGACGACGTC 60
2b 103 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCTCCCTGGAGATCCACCCCGACGACGTC 162
2Y 61 TTGAGGCTGTGTGTATCTACCTTCTGGAGCCCTCTAGCCCGAGCTCTGCG 120
2b 163 TTGAGGCTGTGTGTATCTACCTTCTGGAGCCCTCTAGCCCGAGCTCTGCG 222
2Y 121 TCTCTCAAGGAGGACGAGTACCCAGTGGGTCTCCAGTGTCTGCCCAAGTGACGTCAGGT 180
2b 223 TCTCTCAAGGAGGACGAGTACCCAGTGGGTCTCCAGTGTCTGCCCAAGTGACGTCAGGT 282
2Y 181 TATCGTGTCAAGGAGGCTCGGGGAGCTACCGGACACAGTGTGTCAACCTGCCCTCCA 240
2b 283 TATCGTGTCAAGGAGGCTCGGGGAGCTACCGGACACAGTGTGTGTGTGTGTGTGTGTGT 342
2Y 241 GGCACCTCATTTGCCCACTCAATGGGCTTAAGCAAGTGTCTGACGTGCCAAATGTGTGAC 300

Db 343 GGCACCTACATTTGCCCACTCAATGGGCTTAAGCAAGTGTCTGACGTGCCAAATGTGTGAC 402
QY 301 CCAGCATGGGCTGGCGGAGCGGAGCGGAACTCTCCAGACAGAGAGCGCGTGTGTGGC 360
Db 403 CCAGCATGGGCTGGCGGAGCGGAGCGGAACTCTCTCAGACAGAGACCGCGTGTGTGGC 462
QY 361 TGCAGCCAGCGCACTTTCTGATCTGCTCCAGGACGGGACCACTGCGCGCGCTGCGCGCT 420
Db 463 TGCAGCCAGCGCACTTTCTGATCTGCTCCAGGACGGGACCACTGCGCGCGCTGCGCGCT 522
QY 421 TACGCCACCTCCAGCGCGGCGGAGCGGTGCAAGAGGAGGACCGAGAGTCAGACACC 480
Db 523 TACGCCACCTCCAGCGCGGCGGAGCGGTGCAAGAGGAGGACCGAGAGTCAGACACC 582
QY 481 CTGTGTGAGAACTGCCCGCGGCGGACCTTCTTCCAAATGGGACCTCGAGGAATGTGAG 540
Db 583 CTGTGTGAGAACTGCCCGCGGCGGACCTTCTTCCAAATGGGACCTCGAGGAATGTGAG 642
QY 541 CACCAGACCAATTTG 554
Db 643 CACCAGACCAATTTG 656

RESULT 15

ABX90577

ID ABX90577 standard; cDNA; 1834 BP.

XX AC ABX90577;

XX DT 06-MAY-2003 (first entry)

XX DE Human membrane-bound Herpesvirus Entry Mediator-2 (mhVEM-2) cDNA.

XX KW Human; ss; Gene; TANGO-69 receptor; herpesvirus entry mediator; HVEM;
KW SHVEM1; SHVEM2; SHVEM3; mhVEM2; tumour necrosis factor receptor; TNFR;
KW immune disorder; autoimmune disorder; arthritis; graft rejection;
KW T-cell disorder; AIDS; inflammatory disorder; bacterial infection;
KW psoriasis; septicemia; cerebral malaria; inflammatory bowel disease;
KW rheumatoid arthritis; osteoarthritis; allergic inflammatory disorder;
KW asthma; psoriasis; apoptotic disorder; rheumatoid arthritis;
KW systemic lupus erythematosus; insulin-dependent diabetes mellitus;
KW cytotoxic disorder; septic shock; cachexia; proliferative disorder;
KW B-cell cancer.

XX KW Homo sapiens.

XX OS US2002132297-A1.

XX PN 19-SEP-2002.

XX PD 21-AUG-2001; 2001US-00934289.

XX PF 03-SEP-1998; 98US-00146950.

XX PR (MILL-) MILLENNIUM PHARM INC.

XX PA Busfield SJ;

XX PI WPI; 2003-255106/25.

XX XX P-PSDB; ABU0694.

XX DR New TANGO-69 receptor polynucleotides and polypeptides, useful for

XX PT treating arthritis, graft rejection, AIDS, bacterial infection,

XX PT psoriasis, septicemia, cerebral malaria, inflammatory bowel disease,

XX PT asthma, psoriasis, lupus.

XX PS Claim 2; Fig 7; 79pp; English.

XX CC The invention relates to an isolated nucleic acid molecule, designated as

XX CC TANGO-69 receptor polynucleotide. TANGO-69 receptor refers to a portion

XX CC of the proteins SHVEM1, SHVEM2, SHVEM3 and mhVEM2 (where HVEM is

XX CC Herpesvirus Entry Mediator and "s" refers to a soluble form and "m" to a

membrane bound form). Also included are a host cell containing TANGO-69 receptor nucleic acid, a non-human mammalian host cell containing TANGO-69 receptor nucleic acid, an isolated polypeptide that is encoded by TANGO-69 receptor nucleic acid, an antibody that selectively binds to the TANGO-69 receptor polypeptide, and identifying a compound that binds to and/or modulates the activity of the TANGO-69 receptor polypeptide. The polynucleotides, polypeptides compounds and methods are useful for treating immune disorders such as autoimmune disorders (e.g. arthritis, graft rejection), T-cell disorders (AIDS), inflammatory disorders (e.g. bacterial infection, psoriasis, septicemia, cerebral malaria, inflammatory bowel disease, rheumatoid arthritis, osteoarthritis), allergic inflammatory disorders (e.g. asthma, psoriasis), apoptotic disorders (e.g. rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock, cachexia, and proliferative disorders (e.g. B-cell cancers). TANGO-69 receptor is a member of the TNF (tumour necrosis factor) superfamily of proteins. The present sequence encodes a TANGO-69 receptor protein

Sequence 1834 BP; 398 A; 555 C; 540 G; 341 T; 0 U; 0 Other;

Query Match 93.2%; Score 550.8; DB 7; Length 1834;
Best Local Similarity 99.8%; Pred. No. 1.2e-129; Indels 0; Gaps 0;
Matches 552; Conservative 0; Mismatches 2;

1 ATGGAGCCTCTCGAGACTGGGGCTCTCTCTCTGAGATCCACCCCGAGAACCGAGCTC 60
103 ATGGAGCCTCTCGAGACTGGGGCTCTCTCTCTGAGATCCACCCCGAGAACCGAGCTC 162
61 TTGAGGCTGTGTATCTACCTTTCTGGAGCCCTCTAGCCCGAGCTCTGGCG 120
163 TTGAGGCTGTGTATCTACCTTTCTGGAGCCCTCTAGCCCGAGCTCTGGCG 222
121 TCCTGCAAGGAGACAGTAGTACCCAGTGGGCTCCAGTGTGCCCCCAAGTGCAGTCCAGGT 180
223 TCCTGCAAGGAGACAGTAGTACCCAGTGGGCTCCAGTGTGCCCCCAAGTGCAGTCCAGGT 282
181 TATCGTGTGAAGAGGCTCTCGGGAGCTGACGGGCAAGTGTGTGAACCTTGCCTTCA 240
283 TATCGTGTGAAGAGGCTCTCGGGAGCTGACGGGCAAGTGTGTGAACCTTGCCTTCA 342
241 GGCACCTACATTGCCACCTCAATGGCTAAGCAAGTGTGTGAGTGCACCAATGTGTGAC 300
343 GGCACCTACATTGCCACCTCAATGGCTAAGCAAGTGTGTGAGTGCACCAATGTGTGAC 402
301 CCAGCCATGGGCTCTGCGCGAGCCGAACTGTCTCAGGACAGAGAACCGCGTGTGTGC 360
403 CCAGCCATGGGCTCTGCGCGAGCCGAACTGTCTCAGGACAGAGAACCGCGTGTGTGC 462
361 TGCAGCCAGGCCACTTCTGATCGTCCAGGACGGGACCACTGCGCCGCGTGCAGCGCT 420
463 TGCAGCCAGGCCACTTCTGATCGTCCAGGACGGGACCACTGCGCCGCGTGCAGCGCT 522
421 TAGGCCACTCCAGCCCGGCGCAGAGGCTGCAAGGGAGGACCCAGAGTCAAGACAC 480
523 TAGGCCACTCCAGCCCGGCGCAGAGGCTGCAAGGGAGGACCCAGAGTCAAGACAC 582
481 CTGTGTCAAGACTGCCCCCGGGGACCTTCTCTCCAAATGGGACCTTGGAGGATGTGAG 540
583 CTGTGTCAAGACTGCCCCCGGGGACCTTCTCTCCAAATGGGACCTTGGAGGATGTGAG 642
541 CACCAAGCAATTG 554
643 CACCAAGCAAGTG 656

ult No.	Query No.	Score	Match	Length	DB	ID	Description
1	591	100.0	591	3	US-09-146-950-19	Sequence 19, Appl	
2	591	100.0	1596	3	US-09-146-950-17	Sequence 17, Appl	
3	582.6	93.5	4622	3	US-08-509-024-6	Sequence 6, Appl	
4	582.6	93.5	4622	4	US-09-333-279-6	Sequence 6, Appl	
5	582.6	93.5	4622	4	US-09-631-780-6	Sequence 6, Appl	
6	580.8	93.2	1724	3	US-08-509-034-1	Sequence 1, Appl	
7	580.8	93.2	1724	4	US-09-333-279-1	Sequence 1, Appl	
8	580.8	93.2	1724	4	US-09-631-780-1	Sequence 1, Appl	
9	550	93.1	579	3	US-09-146-950-3	Sequence 3, Appl	
10	550	93.1	1929	3	US-09-146-950-1	Sequence 1, Appl	
11	544.4	92.1	1724	5	PCR-US96-12374-1	Sequence 1, Appl	
12	340.2	57.6	976	4	US-09-016-434-937	Sequence 937, Appl	
13	114	19.3	114	3	US-09-146-950-22	Sequence 22, Appl	
14	112.4	19.0	114	3	US-09-146-950-6	Sequence 6, Appl	
15	61.2	10.4	691	1	US-08-266-080B-12	Sequence 12, Appl	
16	61.2	10.4	691	5	PCR-US95-05423-12	Sequence 12, Appl	
17	61.2	10.4	705	4	US-09-328-394-3	Sequence 3, Appl	
18	59.6	10.1	705	4	US-09-580-235-3	Sequence 3, Appl	
19	59.6	10.1	705	4	US-09-580-235-7	Sequence 7, Appl	
20	59.6	10.1	705	4	US-09-580-181-3	Sequence 3, Appl	
21	59.6	10.1	705	4	US-09-580-181-7	Sequence 7, Appl	
22	59.6	10.1	705	4	US-09-102-530-3	Sequence 3, Appl	
23	59.6	10.1	705	4	US-09-102-530-7	Sequence 7, Appl	
24	59.6	10.1	1557	1	US-08-385-229-3	Sequence 3, Appl	
25	59.6	10.1	1557	4	US-09-579-845-2	Sequence 2, Appl	
26	59.6	10.1	1641	1	US-08-385-229-1	Sequence 1, Appl	
27	59.6	10.1	1641	2	US-08-650-000-1	Sequence 1, Appl	

421 TAGCCACCTCCAGCCCGGSCCAGAGGGTGCAGAGGAGGACCGAGAGTCCAGACACC 480
421 TAGCCACCTCCAGCCCGGSCCAGAGGGTGCAGAGGAGGACCGAGAGTCCAGACACC 480
481 CTGTGTGAGAACTGCCCCCGGCGGACCTTCTCCCAATGGGACCTGGAGGAATGTGAG 540
481 CTGTGTGAGAACTGCCCCCGGCGGACCTTCTCCCAATGGGACCTGGAGGAATGTGAG 540
541 CACCAGACCAATTGGCCTAATCATATATGTGTGAAAGAGAAAGCAAGGGG 591
541 CACCAGACCAATTGGCCTAATCATATATGTGTGAAAGAGAAAGCAAGGGG 591

SULT 2

-09-146-950-17

Sequence 17, Application US/09146950A

Patent No. 6287808

GENERAL INFORMATION:

APPLICANT: Busfield, Samantha J.

TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 09404/057001

CURRENT APPLICATION NUMBER: US/09/146,950A

CURRENT FILING DATE: 1998-09-03

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 17

LENGTH: 1596

TYPE: DNA

ORGANISM: Homo sapiens

-09-146-950-17

Query Match 100.0%; Score 591; DB 3; Length 1596;
Best Local Similarity 100.0%; Pred. No. 2,6e-147; Indels 0; Gaps 0;
Matches 591; Conservative 0; Mismatches 0

1 ATGAGGCTCTCGAGACTGGGGCCCTCTCCCTGGAGATCCACCCCGACGACGTC 60
107 ATGAGGCTCTCGAGACTGGGGCCCTCTCCCTGGAGATCCACCCCGACGACGTC 166
61 TTGAGGCTGGTGTATCTACCTTTCTGGAGCCCCCTGTACGCCCGCAGCTCTGCCG 120
167 TTGAGGCTGGTGTATCTACCTTTCTGGAGCCCCCTGTACGCCCGCAGCTCTGCCG 226
121 TCCTCCAAAGGAGGACGATACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCAGTCCAGT 180
227 TCCTCCAAAGGAGGACGATACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCAGTCCAGT 286
181 TATCGTGTGAAGAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTAACCTGCCCTCCA 240
287 TATCGTGTGAAGAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTAACCTGCCCTCCA 346
241 GGCACCTACATTGCCCACTCAATGGGCTAAGCAAGTGTCTGCAGTGCCCAAAATGTGTGAC 300
347 GGCACCTACATTGCCCACTCAATGGGCTAAGCAAGTGTCTGCAGTGCCCAAAATGTGTGAC 406
301 CCAGCCATGGGCTCGGGGAGCGGAACTGTCTCAGGACAGAGAAACGCGCTGTGTGAC 360
407 CCAGCCATGGGCTCGGGGAGCGGAACTGTCTCAGGACAGAGAAACGCGCTGTGTGAC 466
361 TGCAGCCAGGACCTTCTGATCGTCCAGGACGGGACCACTGCGCGCGGTGCGCGCT 420
467 TGCAGCCAGGACCTTCTGATCGTCCAGGACGGGACCACTGCGCGCGGTGCGCGCT 526
421 TACGCCACCTCCAGCCCGGCGAGAGGTGTCAGAGGAGGACACCGAGAGTCCAGGACACC 480
527 TACGCCACCTCCAGCCCGGCGAGAGGTGTCAGAGGAGGACACCGAGAGTCCAGGACACC 586
481 CTGTGTGAGAACTGCCCCCGGCGGACCTTCTCCCAATGGGACCTGGAGGAATGTGAG 540
587 CTGTGTGAGAACTGCCCCCGGCGGACCTTCTCCCAATGGGACCTGGAGGAATGTGAG 646

QY 541 CACCAGACCAATTGGCCTAATCATATATGTGTGAAAGAGAAAGCAAGGGG 591
Db 647 CACCAGACCAATTGGCCTAATCATATATGTGTGAAAGAGAAAGCAAGGGG 697

RESULT 3

US-08-509-024-6

Sequence 6, Application US/08509024B

Patent No. 6281207

GENERAL INFORMATION:

APPLICANT: SPEAR, Patricia G.

APPLICANT: MONTGOMERY, Rebecca I.

TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN

FILE REFERENCE: 0290-1

CURRENT APPLICATION NUMBER: US/08/509,024B

CURRENT FILING DATE: 1995-07-25

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 6

LENGTH: 4622

TYPE: DNA

ORGANISM: Homo sapiens

US-08-509-024-6

Query Match 93.5%; Score 552.6; DB 3; Length 4622;
Best Local Similarity 98.4%; Pred. No. 5.3e-137;
Matches 558; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

1 ATGAGGCTCTCGAGACTGGGGCCCTCTCCCTGGAGATCCACCCCGACGACGTC 60
64 ATGAGGCTCTCGAGACTGGGGCCCTCTCCCTGGAGATCCACCCCGACGACGTC 123
61 TTGAGGCTGGTGTATCTACCTTTCTGGAGCCCCCTGTACGCCCGCAGTCTGCCG 120
124 TTGAGGCTGGTGTATCTACCTTTCTGGAGCCCCCTGTACGCCCGCAGTCTGCCG 183
121 TCCTGCAAGGAGACGAGTACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCAGTCCAGT 180
184 TCCTGCAAGGAGACGAGTACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCAGTCCAGT 243
181 TATCGTGTGAAGAGGAGCTGCGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 240
244 TATCGTGTGAAGAGGAGCTGCGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 303
241 GGCACCTACATTGCCCACTCAATGGGCTAAGCAAGTGTCTGCAGTGCCCAAAATGTGTGAC 300
304 GGCACCTACATTGCCCACTCAATGGGCTAAGCAAGTGTCTGCAGTGCCCAAAATGTGTGAC 363
301 CCAGCCATGGGCTCGCGCGAGCCGGAACCTGTCCAGGACAGAGAAACGCGCTGTGTGAC 360
364 CCAGCCATGGGCTCGCGCGAGCCGGAACCTGTCCAGGACAGAGAAACGCGCTGTGTGAC 423
361 TGCAGCCAGGACCTTCTGATCGTCCAGGACGGGACCACTGCGCGCGGTGCGCGCT 420
424 TGCAGCCAGGACCTTCTGATCGTCCAGGACGGGACCACTGCGCGCGGTGCGCGCT 483
421 TACGCCACCTCCAGCCCGGCGCAGAGGTCAGAGAGGAGGACACCGAGAGTCCAGGACACC 480
484 TACGCCACCTCCAGCCCGGCGCAGAGGTCAGAGAGGAGGACACCGAGAGTCCAGGACACC 543
481 CTGTGTGAGAACTGCCCCCGGCGGACCTTCTCCCAATGGGACCTGGAGGAATGTGAG 540
544 CTGTGTGAGAACTGCCCCCGGCGGACCTTCTCCCAATGGGACCTGGAGGAATGTGAG 603
541 CACCAGACCAATTGGCCTAATCATATG 567
604 CACCAGACCAATTGGCCTAATCATG 630

RESULT 4

US-09-333-279-6

Sequence 6, Application US/09333279

Patent No. 6303336

GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/333,279
CURRENT FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
EQ ID NO 6
LENGTH: 4622
TYPE: DNA
ORGANISM: Homo sapiens
09-333-279-6

Query Match 93.5%; Score 552.6; DB 4; Length 4622;
Best Local Similarity 98.4%; Pred. No. 5.3e-137;
Matches 558; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

1 ATGAGGCTCTCTGGAGACTGGGGCTCTCTCTCTGGAGATCCACCCCGAGAACCGACGTC 60
64 ATGAGGCTCTCTGGAGACTGGGGCTCTCTCTCTGGAGATCCACCCCGAGAACCGACGTC 123

61 TTGAGGCTGGTGTATCTCACTTTCTGGAGAGCCCTCTCTCTGGAGATCCACCCCGAGAACCGACGTC 120
124 TTGAGGCTGGTGTATCTCACTTTCTGGAGAGCCCTCTCTCTGGAGATCCACCCCGAGAACCGACGTC 183

121 TCCTGCAAGGAGGACGAGTACCACTTTCTGGAGAGCCCTCTCTCTGGAGATCCACCCCGAGAACCGACGTC 180
184 TCCTGCAAGGAGGACGAGTACCACTTTCTGGAGAGCCCTCTCTCTGGAGATCCACCCCGAGAACCGACGTC 243

181 TATCGTGTGAAGGAGGCTCTCTCTCTGGAGAGCCCTCTCTCTGGAGATCCACCCCGAGAACCGACGTC 240
244 TATCGTGTGAAGGAGGCTCTCTCTCTGGAGAGCCCTCTCTCTGGAGATCCACCCCGAGAACCGACGTC 303

241 GGACCTACATTTGCCACCTCAATGGCTTAAGCAAGTGTCTGAGTGCACAAATGTGTGAC 300
304 GGACCTACATTTGCCACCTCAATGGCTTAAGCAAGTGTCTGAGTGCACAAATGTGTGAC 363

301 CCAGCCATGGGCTCTGGAGAGCCGAGAACTGTCTCAAGGACAGAGAACCGCGTGTGTGGC 360
364 CCAGCCATGGGCTCTGGAGAGCCGAGAACTGTCTCAAGGACAGAGAACCGCGTGTGTGGC 423

361 TGCAGCCAGGACCTCTCTCTCTGGAGAGCCGAGAACTGTCTCAAGGACAGAGAACCGCGTGTGTGGC 420
424 TGCAGCCAGGACCTCTCTCTCTGGAGAGCCGAGAACTGTCTCAAGGACAGAGAACCGCGTGTGTGGC 483

421 TACGCCACCTCCAGCCCGGAGAGAGGTCAGAGAGGAGGACCGAGAGTCAAGACACC 480
484 TACGCCACCTCCAGCCCGGAGAGAGGTCAGAGAGGAGGACCGAGAGTCAAGACACC 543

481 CTGTGTCAAGTGCCTCTCTCTCTGGAGAGCCGAGAACTGTCTCAAGGACAGAGAACCGCGTGTGTGGC 540
544 CTGTGTCAAGTGCCTCTCTCTCTGGAGAGCCGAGAACTGTCTCAAGGACAGAGAACCGCGTGTGTGGC 603

SUIT 5
-09-631-780-6
Sequence 6, Application US/09631780
Patent No. 6573058
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/631,780
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US/08/509,024B
PRIOR FILING DATE: 1995-07-25

NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 4622
TYPE: DNA
ORGANISM: Homo sapiens
US-09-631-780-6

Query Match 93.5%; Score 552.6; DB 4; Length 4622;
Best Local Similarity 98.4%; Pred. No. 5.3e-137;
Matches 558; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

1 ATGAGGCTCTCTGGAGACTGGGGCTCTCTCTCTGGAGATCCACCCCGAGAACCGACGTC 60
64 ATGAGGCTCTCTGGAGACTGGGGCTCTCTCTCTGGAGATCCACCCCGAGAACCGACGTC 123

61 TTGAGGCTGGTGTATCTCACTTTCTGGAGAGCCCTCTCTCTGGAGATCCACCCCGAGAACCGACGTC 120
124 TTGAGGCTGGTGTATCTCACTTTCTGGAGAGCCCTCTCTCTGGAGATCCACCCCGAGAACCGACGTC 183

121 TCCTGCAAGGAGGACGAGTACCACTTTCTGGAGAGCCCTCTCTCTGGAGATCCACCCCGAGAACCGACGTC 180
184 TCCTGCAAGGAGGACGAGTACCACTTTCTGGAGAGCCCTCTCTCTGGAGATCCACCCCGAGAACCGACGTC 243

181 TATCGTGTGAAGGAGGCTCTCTCTCTGGAGAGCCCTCTCTCTGGAGATCCACCCCGAGAACCGACGTC 240
244 TATCGTGTGAAGGAGGCTCTCTCTCTGGAGAGCCCTCTCTCTGGAGATCCACCCCGAGAACCGACGTC 303

241 GGACCTACATTTGCCACCTCAATGGCTTAAGCAAGTGTCTGAGTGCACAAATGTGTGAC 300
304 GGACCTACATTTGCCACCTCAATGGCTTAAGCAAGTGTCTGAGTGCACAAATGTGTGAC 363

301 CCAGCCATGGGCTCTGGAGAGCCGAGAACTGTCTCAAGGACAGAGAACCGCGTGTGTGGC 360
364 CCAGCCATGGGCTCTGGAGAGCCGAGAACTGTCTCAAGGACAGAGAACCGCGTGTGTGGC 423

361 TGCAGCCAGGACCTCTCTCTCTGGAGAGCCGAGAACTGTCTCAAGGACAGAGAACCGCGTGTGTGGC 420
424 TGCAGCCAGGACCTCTCTCTCTGGAGAGCCGAGAACTGTCTCAAGGACAGAGAACCGCGTGTGTGGC 483

421 TACGCCACCTCCAGCCCGGAGAGAGGTCAGAGAGGAGGACCGAGAGTCAAGACACC 480
484 TACGCCACCTCCAGCCCGGAGAGAGGTCAGAGAGGAGGACCGAGAGTCAAGACACC 543

481 CTGTGTCAAGTGCCTCTCTCTCTGGAGAGCCGAGAACTGTCTCAAGGACAGAGAACCGCGTGTGTGGC 540
544 CTGTGTCAAGTGCCTCTCTCTCTGGAGAGCCGAGAACTGTCTCAAGGACAGAGAACCGCGTGTGTGGC 603

RESULT 6
US-08-509-024-1
Sequence 1, Application US/08509024B
Patent No. 6291207
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/08/509,024B
CURRENT FILING DATE: 1995-07-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1724
TYPE: DNA
ORGANISM: Homo sapiens
US-08-509-024-1

Query Match 93.2%; Score 550.8; DB 3; Length 1724;

Best Local Similarity 99.6%; Pred. No. 1.2e-136; Mismatches 2; Indels 0; Gaps 0;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGAGGCTCTCTGAGACTGGGGGCTCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 60
294 ATGAGGCTCTCTGAGACTGGGGGCTCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 353
61 TTGAGGCTCTCTGAGACTGGGGGCTCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 120
354 TTGAGGCTCTCTGAGACTGGGGGCTCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 413
121 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCAGTGTGCTGCAAGTGCAGTCCAGGT 180
414 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCAGTGTGCTGCAAGTGCAGTCCAGGT 473
181 TATCGTGTGAAGAGGCTCTGGGGAGCTGACGGGACAGTGTGTGAACCCCTGCTCCA 240
474 TATCGTGTGAAGAGGCTCTGGGGAGCTGACGGGACAGTGTGTGAACCCCTGCTCCA 533
241 GGCACCTACATTGCCACCTCAATGCGCTTAAGCAAGTGTCTGCAAGTGCACAAATGTGTGAC 300
534 GGCACCTACATTGCCACCTCAATGCGCTTAAGCAAGTGTCTGCAAGTGCACAAATGTGTGAC 593
301 CCAGCCATGGGCTCTGGGGAGCTGACGGGACAGTGTGCTGCAAGTGCACAAATGTGTGAC 360
594 CCAGCCATGGGCTCTGGGGAGCTGACGGGACAGTGTGCTGCAAGTGCACAAATGTGTGAC 653
361 TGCAGCCAGGCTCTGGGGAGCTGACGGGACAGTGTGCTGCAAGTGCACAAATGTGTGAC 420
654 TGCAGCCAGGCTCTGGGGAGCTGACGGGACAGTGTGCTGCAAGTGCACAAATGTGTGAC 713
421 TACGCCACCTCCAGCCGCGGAGCTGACGGGACAGTGTGCTGCAAGTGCACAAATGTGTGAC 480
714 TACGCCACCTCCAGCCGCGGAGCTGACGGGACAGTGTGCTGCAAGTGCACAAATGTGTGAC 773
481 CTGTGTGAGAACTGCCCCCGGAGCTTCTCTCCCAATGGGAGCCCTGGAGGAATGTGAG 540
774 CTGTGTGAGAACTGCCCCCGGAGCTTCTCTCCCAATGGGAGCCCTGGAGGAATGTGAG 833
541 CACCAGACCAATTG 554
834 CACCAGACCAATTG 847

RESULT 7
3-09-333-279-1
Sequence 1, Application US/09333279
Patent No. 6303336
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/333,279
PRIOR APPLICATION NUMBER: 1999-06-15
CURRENT FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1724
TYPE: DNA
ORGANISM: Homo sapiens
S-09-333-279-1

Query Match 93.2%; Score 550.8; DB 4; Length 1724;
Best Local Similarity 99.6%; Pred. No. 1.2e-136;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGAGGCTCTCTGAGACTGGGGGCTCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 60
294 ATGAGGCTCTCTGAGACTGGGGGCTCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 353
61 TTGAGGCTCTCTGAGACTGGGGGCTCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 120

Db Qy 354 TTGAGGCTGTGTGTATCTCACCCTTCTGGGAGCCCTGCTACGCCCCAGCTCTGCGG 413
Qy 121 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCGAGTGTGCTGCCCAAGTGCAGTCCAGGT 180
Db 414 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCGAGTGTGCTGCCCAAGTGCAGTCCAGGT 473
Qy 181 TATCGTGTGAAGAGGCTCTGGGGAGCTGACGGGACAGTGTGTGAACCCCTGCTCCA 240
Db 474 TATCGTGTGAAGAGGCTCTGGGGAGCTGACGGGACAGTGTGTGAACCCCTGCTCCA 533
Qy 241 GGCACCTACATTGCCACCTCAATGCGCTTAAGCAAGTGTCTGCAAGTGCACAAATGTGTGAC 300
Db 534 GGCACCTACATTGCCACCTCAATGCGCTTAAGCAAGTGTCTGCAAGTGCACAAATGTGTGAC 593
Qy 301 CCAGCCATGGGCTCTGGGGAGCTGACGGGACAGTGTGCTGCAAGTGCACAAATGTGTGAC 360
Db 594 CCAGCCATGGGCTCTGGGGAGCTGACGGGACAGTGTGCTGCAAGTGCACAAATGTGTGAC 653
Qy 361 TGCAGCCAGGCTCTGGGGAGCTGACGGGACAGTGTGCTGCAAGTGCACAAATGTGTGAC 420
Db 654 TGCAGCCAGGCTCTGGGGAGCTGACGGGACAGTGTGCTGCAAGTGCACAAATGTGTGAC 713
Qy 421 TACGCCACCTCCAGCCGCGGAGCTGACGGGACAGTGTGCTGCAAGTGCACAAATGTGTGAC 480
Db 714 TACGCCACCTCCAGCCGCGGAGCTGACGGGACAGTGTGCTGCAAGTGCACAAATGTGTGAC 773
Qy 481 CTGTGTGAGAACTGCCCCCGGAGCTTCTCTCCCAATGGGAGCCCTGGAGGAATGTGAG 540
Db 774 CTGTGTGAGAACTGCCCCCGGAGCTTCTCTCCCAATGGGAGCCCTGGAGGAATGTGAG 833
Qy 541 CACCAGACCAATTG 554
Db 834 CACCAGACCAATTG 847

RESULT 8
US-09-631-780-1
Sequence 1, Application US/09631780
Patent No. 6573058
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/631,780
PRIOR APPLICATION NUMBER: 2000-08-03
CURRENT FILING DATE: 2000-08-03
PRIOR FILING DATE: 1995-07-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1724
TYPE: DNA
ORGANISM: Homo sapiens
US-09-631-780-1

Query Match 93.2%; Score 550.8; DB 4; Length 1724;
Best Local Similarity 99.6%; Pred. No. 1.2e-136;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGAGGCTCTCTGAGACTGGGGGCTCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 60
294 ATGAGGCTCTCTGAGACTGGGGGCTCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 353
61 TTGAGGCTCTCTGAGACTGGGGGCTCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 120
354 TTGAGGCTCTCTGAGACTGGGGGCTCTCTCTCTGGAGATCCACCCCGAAGCCGACGTC 413
121 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCGAGTGTGCTGCCCAAGTGCAGTCCAGGT 180
414 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCGAGTGTGCTGCCCAAGTGCAGTCCAGGT 473
181 TATCGTGTGAAGAGGCTCTGGGGAGCTGACGGGACAGTGTGTGAACCCCTGCTCCA 240

474 TATCGTGTGAAGAGGCGCTGGGGGAGCTGACGGGCAAGTGTGAACCTGCGCTCCA 533
241 GGCACCTACATGGCCCACTCAATGGCTTAAGCAAGTGTCTGCAAGTGCCTGCAATGTGTGAC 300
534 GGCACCTACATGGCCCACTCAATGGCTTAAGCAAGTGTCTGCAAGTGCCTGCAATGTGTGAC 593
301 CCAGCCATGGGCGCTGGCGGCGAGCGGAACTGCTCCAGGACAGAGAACGGCGTGTGTGGC 360
594 CCAGCCATGGGCGCTGGCGGCGAGCGGAACTGCTCCAGGACAGAGAACGGCGTGTGTGGC 653
361 TGCAGCCAGGCGCACTTTCGATCTCCAGACGGGACCACTGCGCGGCGTGTGGCGCT 420
654 TGCAGCCAGGCGCACTTTCGATCTCCAGACGGGACCACTGCGCGGCGTGTGGCGCT 713
421 TAGCCCACTCCAGCCCGGCGGCGAGGGGTGCAGAGGGAGGACCGGAGTCCAGGACACC 480
714 TAGCCCACTCCAGCCCGGCGGCGAGGGGTGCAGAGGGAGGACCGGAGTCCAGGACACC 773
481 CTGTGTCAAGAACTGGCCCGGCGGACCTTCTCTCCAAATGGGACCCCTGGAGGAATGTGAC 540
774 CTGTGTCAAGAACTGGCCCGGCGGACCTTCTCTCCAAATGGGACCCCTGGAGGAATGTGAC 833
541 CACCAGACCAATGTG 554
834 CACCAGACCAATGTG 847

JUL 9
-09-146-950-3
Sequence 3, Application US/09146950A
Patent No. 6287808
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 579
TYPE: DNA
ORGANISM: Homo sapiens
-09-146-950-3

Query Match 93.1%; Score 550; DB 3; Length 579;
Best Local Similarity 99.1%; Pred. No. 1.4e-136;
Matches 553; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGACCGACGTC 60
1 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGACCGACGTC 60
61 TTGAGGCTGTGTATCTCACTTCTGGAGCCCTCTGTCAGCCCAAGCTGTGCG 120
61 TTGAGGCTGTGTATCTCACTTCTGGAGCCCTCTGTCAGCCCAAGCTGTGCG 120
121 TCTGCAAGGAGACAGTACCAAGTGGGCTCGAGTGTGCGGCAAGTGCAGTCCAGT 180
121 TCTGCAAGGAGACAGTACCAAGTGGGCTCGAGTGTGCGGCAAGTGCAGTCCAGT 180
181 TATCGTGTGAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTGGCCCTCA 240
181 TATCGTGTGAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTGGCCCTCA 240
241 GGCACCTACATTGCCCACTCAATGGCCTTAAGCAAGTGTCTGCAAGTGCCTGTCAC 300
241 GGCACCTACATTGCCCACTCAATGGCCTTAAGCAAGTGTCTGCAAGTGCCTGTCAC 300
301 CCAGCCATGGGCGCTGGCGGCGGACCTGCTCCAGGACAGAGAACCCCTGTGTGGC 360

Db 301 CCAGCCATGGGCGCTGGCGGCGGAGCGGAACTGCTCCAGGACAGAGAACCCCTGTGTGGC 360
QY 361 TGCAGCCAGGCGCACTTTCGATCTCCAGACGGGACCACTGCGCGGCGTGTGGCGCT 420
Db 361 TGCAGCCAGGCGCACTTTCGATCTCCAGACGGGACCACTGCGCGGCGTGTGGCGCT 420
QY 421 TACGCCCACTCCAGCCCGGCGGCGAGGGGTGCAGAGGGAGGACCGGAGTCCAGGACACC 480
Db 421 TACGCCCACTCCAGCCCGGCGGCGAGGGGTGCAGAGGGAGGACCGGAGTCCAGGACACC 480
QY 481 CTGTGTCAAGAACTGGCCCGGCGGACCTTCTCTCCAAATGGGACCCCTGGAGGAATGTGAC 540
Db 481 CTGTGTCAAGAACTGGCCCGGCGGACCTTCTCTCCAAATGGGACCCCTGGAGGAATGTGAC 540
QY 541 CACCAGACCAATGTGCGCT 558
Db 541 CACCAGACCAATGTGCGCT 558

RESULT 10
US-09-146-950-1
Sequence 1, Application US/09146950A
Patent No. 6287808
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1929
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (297)...(875)
US-09-146-950-1

Query Match 93.1%; Score 550; DB 3; Length 1929;
Best Local Similarity 99.1%; Pred. No. 2e-136;
Matches 553; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGACCGACGTC 60
Db 297 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGACCGACGTC 356
QY 61 TTGAGGCTGTGTATCTCACTTCTGGAGCCCTCTGTCAGCCCAAGCTGTGCG 120
Db 357 TTGAGGCTGTGTATCTCACTTCTGGAGCCCTCTGTCAGCCCAAGCTGTGCG 416
QY 121 TCTGCAAGGAGACAGTACCAAGTGGGCTCGAGTGTGCGGCAAGTGCAGTCCAGT 180
Db 417 TCTGCAAGGAGACAGTACCAAGTGGGCTCGAGTGTGCGGCAAGTGCAGTCCAGT 476
QY 181 TATCGTGTGAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTGGCCCTCA 240
Db 477 TATCGTGTGAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTGGCCCTCA 536
QY 241 GGCACCTACATTGCCCACTCAATGGCCTTAAGCAAGTGTCTGCAAGTGCCTGTCAC 300
Db 537 GGCACCTACATTGCCCACTCAATGGCCTTAAGCAAGTGTCTGCAAGTGCCTGTCAC 596
QY 301 CCAGCCATGGGCGCTGGCGGCGGAGCGGAACTGCTCCAGGACAGAGAACCCCTGTGTGGC 360
Db 597 CCAGCCATGGGCGCTGGCGGCGGAGCGGAACTGCTCCAGGACAGAGAACCCCTGTGTGGC 656
QY 361 TGCAGCCAGGCGCACTTTCGATCTCCAGGACGGGACCACTGCGCGGCGTGTGGC 420
Db 657 TGCAGCCAGGCGCACTTTCGATCTCCAGGACGGGACCACTGCGCGGCGTGTGGC 716

Y 421 TAGCCACCTCCAGCCCGGCGCAGAGGCTGAGAGGAGGACCGAGAGTCAGGACACC 480
b 717 TAGCCACCTCCAGCCCGGCGCAGAGGCTGAGAGGAGGACCGAGAGTCAGGACACC 776
Y 481 CTGTGTGAGAACTGCCCCCGGCGCCTTCTCTCCAAATGGGACCTTGAGAGGAATGTGAC 540
b 777 CTGTGTGAGAACTGCCCCCGGCGCCTTCTCTCCAAATGGGACCTTGAGAGGAATGTGAC 836
Y 541 CACCAGACCAATGGCCT 558
b 837 CACCAGACCAACCGAGCT 854

RESULT 11

CT-US96-12374-1

Sequence 1, Application PC/TUS9612374

GENERAL INFORMATION:

APPLICANT: Northwestern University

TITLE OF INVENTION: Herpes Virus Entry Mediator

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Goldsmith, Milnamow & Katz, Ltd.

STREET: 180 N. Stetson, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/12374

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Northrup, Thomas E.

REGISTRATION NUMBER: 33,368

REFERENCE/DOCKET NUMBER: NOR3446P020PC

TELEPHONE: (312) 616-5400

TELEFAX: (312) 616-5460

TELEX: --

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1724 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ANTI-SENSE: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 294..1145

FEATURE:

NAME/KEY: mat peptide

LOCATION: 294..1142

CT-US96-12374-1

Query Match 92.1%; Score 544.4; DB 5; Length 1724;
Best Local Similarity 98.9%; Pred. No. 5.8e-135;
Matches 548; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

2Y 1 ATGAGGCTCTGAGAGTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAGCCGACGTC 60
b 294 ATGAGGCTCTGAGAGTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAGCCGACGTC 353
2Y 61 TTGAGGCTGTGTGTATCTACCTTTCTGGAGCCCCCTGTACGCCAGCTCTGCGG 120
b 354 TTGAGGCTGTGTGTATCTACCTTTCTGGAGCCCCCTGTACGCCAGCTCTGCGG 413
2Y 121 TCCTCAAGGAGGAGGACGAGTCCAGTGGGCTCCGAGTGGCTGCCCAAGTCAGTCCAGGT 180

Db 414 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTCTCCCAAGTCAGTCCAGGT 473
QY 181 TATCGTGTGAGAGGAGCTGCGGGAGCTGACGGGACACAGTGTGAAACCTGCCCTCCA 240
Db 474 TATCGTGTGAGAGGAGCTGCGGGAGCTGACGGGACACAGTGTGAAACCTGCCCTCCA 533
QY 241 GGCACCTACATTGCCCACTCAATGGGCTAAGCAAGTGTGACAGTGCCAAATGTGTGAC 300
Db 534 GGCACCTACATTGCCCACTCAATGGGCTAAGCAAGTGTGACAGTGCCAAATGTGTGAC 593
QY 301 CCAGCCATGGGCTGCGGCGGAGCGGAGTCTCCAGGACAGAGAACCGCTGTGTGGC 360
Db 594 CCAGCCATGGGCTGCGGCGGAGCGGAGTCTCCAGGACAGAGAACCGCTGTGTGGC 653
QY 361 TGCAGCCAGGCGCACTTCTGCATCTCCAGGACGGGACCACTGCGCGGCTGCGCGCT 420
Db 654 TGCAGCCAGGCGCACTTCTGCATCTCCAGGACGGGACCACTGCGCGGCTGCGCGCT 713
QY 421 TAGGCCACTTCAGCCCGGCGGAGGGTGCAGAGGAGGACCGGAGAGTCAGGACACC 480
Db 714 TAGGCCACTTCAGCCCGGCGGAGGGTGCAGAGGAGGACCGGAGAGTCAGGACACC 773
QY 481 CTGTGTGAGAACTGCCCCCGGCGCCTTCTCTCCAAATGGGACCTTGAGAGGAATGTGAC 540
Db 774 CTGTGTGAGAACTGCCCCCGGCGCCTTCTCTCCAAATGGGACCTTGAGAGGAATGTGAC 833
QY 541 CACCAGACCAATGG 554
Db 834 CACCAGACCAAGTG 847

RESULT 12

US-09-016-434-937

Sequence 937, Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young

APPLICANT: Jeffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,434

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 937:

SEQUENCE CHARACTERISTICS:

LENGTH: 976 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: MYONNOT01
CLONE: 778806
09-016-434-937

Query Match 57.6%; Score 340.2; DB 4; Length 976;
 Best Local Similarity 83.2%; Pred. No. 5.7e-81;
 Matches 462; Conservative 0; Mismatches 3; Indels 90; Gaps 3;

1 ATGGAGCCTCTCTGGAGACTGGGGCCTCTCTCTCTGGAGATCCACCCCAAGAACCGAGTC 60
121 ATGGAGCCTCTCTGGAGACTGGGGCCTCTCTCTCTGGAGATCCACCCCAAGAACCGAGTC 180
61 TTGAGGCTGGTGCTGTATCTACCTTTCTGGAGGCCCTCTGTATGCCCCCAAGCTCTGGC 120
181 TTGAGGCTGGTGCTGTATCTACCTTCTCTGGAGGCCCTCTGTATGCCCCCAAGCTCTGGC 240
121 TCTCTCAAGGAGGAGTAGTACCAGTGGGCTCCGAGTGTGCCCCAAGTGAGTCCAGGT 180
241 TCTCTCAAGGAGGAGTAGTACCAGTGGGCTCCGAGTGTGCCCCAAGTGAGTCCAGGT 300
181 TATCTGTGAAGGAGGCTGCGGAGCTGACGGGCAAGTGTGTGAACCTTGCCCTCCA 240
301 TA---TGTGAAGGAGGCTGCGGAGCTGACGGGCAAGTGTGTGTGAACCTTGCCCTCCA 357
241 GGCACCTAATTGGCCCACTCAATGGCTTAAGCAAGTGTCTGACGTGCCAATGTGTAC 300
358 GGCACCTAATTGGCCCACTCAATGGCTTAAGCAAGTGTCTGACGTGCCAATGTGTAC 417
301 CGAGCCTATGGGCTGCGCGCGAGCGGGAATCTCTCCAGACAGAGAACCGCTGTGTGGC 360
418 ----- 417
361 TGCAGCCAGGCCAATTCTGTATGTGTCAAGACGGGACCACTGCGCGGTGCGCGCCT 420
418 -----CCAGGACGGGAGCACTGCGCGGTGCGCGCCT 451
421 TAGCCACCTTCAGCCCGGCGCAGAGGTGACAGAGGAGGACCGACAGAGTCAGAGACAC 480
452 TAGCCACCTTCAGCCCGGCGCAGAGGTGACAGAGGAGGACCGACAGAGTCAGAGACAC 511
481 CTGTGTCAAACTGCCCCCGGGGACC-TTCTCTCCCAATGGGACCTCTGGAGGAATGTCA 539
512 CTGTGTCAAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCTCTGGAGGAATGTCA 571
540 GCACCAGACCAATTG 554
572 GCACCAGACCAAGTG 586

3ULT 13
 -09-146-950-22
 Sequence 22, Application US/09146950A
 Patent No. 6287808
 GENERAL INFORMATION:
 APPLICANT: Busfield, Samantha J.
 TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
 FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
 FILE REFERENCE: 09404/057001
 CURRENT APPLICATION NUMBER: US/09/146,950A
 CURRENT FILING DATE: 1998-09-03
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 22
 LENGTH: 114
 TYPE: DNA
 ORGANISM: Homo sapiens
 -09-146-950-22

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Query Match      19.3%; Score 114; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.4e-21;
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	Matches	114;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	ATGAGGCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCCGAACCGAGCTC	60							
DB	1	ATGAGGCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCCGAACCGAGCTC	60							
QY	61	TTGAGGCTGTGTGTATCTCACTTTCTGGAGCGCCCTCTGTCAGCCCCAGCT	114							
DB	61	TTGAGGCTGTGTGTATCTCACTTTCTGGAGCGCCCTCTGTCAGCCCCAGCT	114							

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RESULT 14
US-09-146-950-6
; Sequence 6, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 114
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-146-950-6

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Query Match	19.0%;	Score	112.4;	DB	3;	Length	114;
Best Local Similarity	99.1%;	Prod.	No. 6.3e-21;				
Matches 113;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps
0;							
QY	1	ATGAGGCTCTCGAGACTGGGGGCTCTCTCTGGAGATCCACCCCGAGACCGAGTC	60				
Db	1	ATGAGGCTCTCGAGACTGGGGGCTCTCTCTGGAGATCCACCCCGAGACCGAGTC	60				
QY		TTGAGGCTGGTGCTGTATCTCACTTTTCTGGAGGCCCTCTCTAGGCCCCAGCT	114				
Db	61	TTGAGGCTGGTGCTGTATCTCACTTTTCTGGAGGCCCTCTCTAGGCCCCAGCT	114				

RESULT 15
 US-08-266-080B-12
 ; Sequence 12, Application US/08266080B
 ; Patent No. 5606031
 ; GENERAL INFORMATION:
 ; APPLICANT: Jack Lile
 ; APPLICANT: Tadahiko Kohno
 ; APPLICANT: Duane Bonam
 ; APPLICANT: Mary S. Rosendahl
 ; TITLE OF INVENTION: Production of Biologically Active
 ; TITLE OF INVENTION: Recombinant Neurotrophic Protein
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Swanson & Bratschun, L.L.C.
 ; STREET: 8400 E. Prentice Avenue, Suite 200
 ; CITY: Englewood
 ; STATE: Colorado
 ; COUNTRY: USA
 ; Zip: 80111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
 ; COMPUTER: IBM compatible
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/266,080B
 ; FILING DATE: 27-JUNE-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/240,122
 ; FILING DATE: 09-MAY-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/680,681
FILING DATE: 04-APRIL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/505,441
FILING DATE: 06-APRIL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: SYNE200CS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 691 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
S-08-266-080B-12

Query Match: 10.4%; Score 61.2; DB 1; Length 691;
Best Local Similarity 50.0%; Pred. No. 3.8e-07;
Matches 181; Conservative 0; Mismatches 178; Indels 3; Gaps 1;

y	156	GTGCTGCCCCAAAGTCAGTCAGGTTATCGTGTGAAGGAGCCCTGCGGGGAGCTGACGGG	215
c	228	GTGCTGCACAAAGTGTGCGCGGCCACATGCAAAAGTCTTCTGTACCAAGACCTCGGA	287
y	216	CACAGTGTGTGAACCTGCGCTCCAGGCACTTACATGTCCTCAATGGCCTAAGCAA	275
b	288	CACCGTGTGTGACTCCTGTGTAGGACAGCACATACACCCAGCTCTGGAAGTGGGTCCCGA	347
y	276	GTGCTGTGAGTCCCAATGTGTGACCCAGCCATGGGCTGCGCGGAGCCGGAACTGCTC	335
c	348	GTGCTTGAGCTGTGG---CTCCCGTGTAGTCTTACCAGGTGAAACTAAGCCTGCAC	404
y	336	CAGGACAGAGAACCGGTGTGTGGTGCAGCCCGCCAGGCCACTTCTGCATCGTCCAGGACGG	395
b	405	TCGGGAACAGAACCGCATCTGCACCTGCAGGCCCGGTGTACTTGGCGCTGAGCAAGCA	464
y	396	GGACCACTGGCGCGGTGCGCGCTTACGCCACTCCAGCCCGGGCCAGAGGGTGCAGAA	455
b	465	GGAGGGGTGCGCGCTGTGTGGCGCCCTGCGCAAGTGCAGGCTGGTGTGCAAGCCCTGTG	524
y	456	GGAGGCACCGAGAGTTCAGGACACCTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCC	515
b	525	ACCAGGAATGAAACATCAGAGTGTGTGCAAGCCCTGTGCCCCGGGAGGTTCTTCAA	584
y	516	CA 517	
b	585	CA 586	

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Job time: 89 secs

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nucleic - nucleic search, using sw model

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(without alignments)
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file: US-09-934-289A-19
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Gapop 10.0 , Gapext 1.0

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tal number of hits satisfying chosen parameters: 5997098

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Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq.*
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6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
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17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	Length	DB	ID	Description
1	591	100.0	591	9	US-09-934-289A-19	Sequence 19, Appl
2	591	100.0	1596	9	US-09-934-289A-17	Sequence 17, Appl
3	52.6	93.5	4622	9	US-09-924-231-6	Sequence 6, Appl
4	50.8	93.2	831	9	US-09-934-289A-43	Sequence 43, Appl
5	50.8	93.2	1724	9	US-09-924-231-1	Sequence 1, Appl
6	50.8	93.2	1724	9	US-09-934-289A-14	Sequence 14, Appl
7	50.8	93.2	1724	16	US-10-369-300-1	Sequence 1, Appl
8	50.8	93.2	1834	9	US-09-934-289A-41	Sequence 41, Appl
9	550	93.1	579	9	US-09-934-289A-3	Sequence 3, Appl
10	550	93.1	1929	9	US-09-934-289A-1	Sequence 1, Appl
11	548.4	92.8	558	9	US-09-934-289A-31	Sequence 31, Appl
12	548.4	92.8	2313	9	US-09-934-289A-29	Sequence 29, Appl
13	547.6	92.7	1704	14	US-10-020-787-1	Sequence 1, Appl
14	340.2	57.6	976	16	US-10-305-720-937	Sequence 937, App

15	259.6	43.9	1082	16	US-10-369-300-3	Sequence 3, Appl
16	233.8	39.6	447	10	US-09-918-595-3536	Sequence 3536, Ap
17	168.8	28.6	350	9	US-09-783-590-11975	Sequence 11975, A
18	126	21.3	126	9	US-09-934-289A-11	Sequence 11, Appl
19	126	21.3	126	9	US-09-934-289A-12	Sequence 12, Appl
20	126	21.3	126	9	US-09-934-289A-27	Sequence 27, Appl
21	126	21.3	126	9	US-09-934-289A-28	Sequence 28, Appl
22	126	21.3	126	9	US-09-934-289A-39	Sequence 39, Appl
23	126	21.3	126	9	US-09-934-289A-40	Sequence 40, Appl
24	126	21.3	126	9	US-09-934-289A-53	Sequence 53, Appl
25	126	21.3	126	9	US-09-934-289A-54	Sequence 54, Appl
26	110.8	18.7	114	9	US-09-934-289A-6	Sequence 6, Appl
27	110.8	18.7	114	9	US-09-934-289A-22	Sequence 22, Appl
28	110.8	18.7	114	9	US-09-934-289A-34	Sequence 34, Appl
29	110.8	18.7	114	9	US-09-934-289A-46	Sequence 46, Appl
30	105	17.8	105	9	US-09-934-289A-10	Sequence 10, Appl
31	105	17.8	105	9	US-09-934-289A-26	Sequence 26, Appl
32	105	17.8	105	9	US-09-934-289A-38	Sequence 38, Appl
33	105	17.8	105	9	US-09-934-289A-52	Sequence 52, Appl
34	62.4	10.6	1968	16	US-10-262-445-122	Sequence 122, App
35	62.4	10.6	1982	9	US-09-907-372-2	Sequence 2, Appl
36	62.4	10.6	1982	10	US-09-917-372-2	Sequence 2, Appl
37	62.4	10.6	2105	16	US-10-369-300-16	Sequence 16, Appl
38	62.4	10.6	2136	9	US-09-962-436-262	Sequence 262, App
39	62.4	10.6	2136	9	US-09-880-107-2135	Sequence 2135, Ap
40	62.4	10.6	2136	9	US-09-954-531-1348	Sequence 1348, Ap
41	62.4	10.6	2136	10	US-09-960-706-634	Sequence 634, App
42	62.4	10.6	2136	10	US-09-873-319-397	Sequence 397, App
43	62.4	10.6	2136	13	US-10-342-887-759	Sequence 759, App
44	62.4	10.6	2136	13	US-10-172-118-759	Sequence 759, App
45	62.4	10.6	2136	16	US-10-159-563-411	Sequence 411, App

ALIGNMENTS

RESULT 1
US-09-934-289A-19
; Sequence 19, Application US/09934289A
; Patent No. US20020132297A1
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE
; TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: MBIO98-061CPC1(M)
; CURRENT APPLICATION NUMBER: US/09/934,289A
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/342,767
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/146,950
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(591)
US-09-934-289A-19

Query Match 100.0%; Score 591; DB 9; Length 591;
Best Local Similarity 100.0%; Pred. No. 9,1e-167; Indels 0; Gaps 0;
Matches 591; Conservative 0; Mismatches 0;
Qy 1 ATGAGGCTCTCGAGACTGGGGGCTCTCTCGAGATCCACCCAGAACCCGACGTC 60
Db 1 ATGAGGCTCTCGAGACTGGGGGCTCTCTCGAGATCCACCCAGAACCCGACGTC 60
Qy 61 TTGAGGCTGTGTGTATCTACCTTCTTGGAGCCCCCTGTAGCCCCAGCTTTCGCG 120

61 TTGAGGCTGGTCTGTATCTCACCTTTCTGGAGCCCTCTGCTACGCCCCAGCTCTGCCG 120
121 TCTTCAGAGGAGGAGTACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCATCCAGGT 180
121 TCTTCAGAGGAGGAGTACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCATCCAGGT 180
181 TATCTGTGAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTCCCTCCA 240
181 TATCTGTGAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTCCCTCCA 240
241 GGCACCTACATTGCCCACTCAATGGCTTAAGCAAGTGTGTGCAGTGCCTCAATGTGAC 300
241 GGCACCTACATTGCCCACTCAATGGCTTAAGCAAGTGTGTGCAGTGCCTCAATGTGAC 300
301 CCAGCCATGGGCTCGCGGAGCGGAGCTGCTCCAGGACAGAGAACCGGTGTGGC 360
301 CCAGCCATGGGCTCGCGGAGCGGAGCTGCTCCAGGACAGAGAACCGGTGTGGC 360
361 TGCAGCCAGGCACTTCTGCATGTCCAGGACGGGACCACTGCGCGGTGCCCGCT 420
361 TGCAGCCAGGCACTTCTGCATGTCCAGGACGGGACCACTGCGCGGTGCCCGCT 420
421 TACGCCACTCCAGCCCGGCGGAGGCTGACAGGAGGACCGAGTCCAGGACACC 480
421 TACGCCACTCCAGCCCGGCGGAGGCTGACAGGAGGACCGAGTCCAGGACACC 480
481 CTGTGTGAGAACTGCCCCCGGGACCTTCTCTCCCAATGGGACCTCGGAGGAATGTGAC 540
481 CTGTGTGAGAACTGCCCCCGGGACCTTCTCTCCCAATGGGACCTCGGAGGAATGTGAC 540
541 CACGAGCAATGGCTTAATCATATGTGTGAAGAAAGCAAGCCAGGGG 591
541 CACGAGCAATGGCTTAATCATATGTGTGAAGAAAGCAAGCCAGGGG 591

RESULT 2

3-09-934-289a-17
Sequence 17, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
FILE REFERENCE: MB1098-061CPIC1(N)
CURRENT APPLICATION NUMBER: US/09/934,289A
CURRENT FILING DATE: 2001-08-21
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 1596
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (107)...(697)
S-09-934-289A-17

Query Match 100.0%; Score 591; DB 9; Length 1596;
Best Local Similarity 100.0%; Pred. No. 1e-166;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCAACCCCGAGAACCGAGTGC 60
107 ATGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCAACCCCGAGAACCGAGTGC 166
61 TTGAGGCTGGTCTGTATCTCACCTTTCTGGAGCCCTCTGCTACGCCCCAGCTCTGCCG 120
167 TTGAGGCTGGTCTGTATCTCACCTTTCTGGAGCCCTCTGCTACGCCCCAGCTCTGCCG 226

QY 121 TCTTCAGAGGAGGAGTACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCATCCAGGT 180
DB 227 TCTTCAGAGGAGGAGTACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCATCCAGGT 286
QY 181 TATCTGTGAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTCCCTCCA 240
DB 287 TATCTGTGAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTCCCTCCA 346
QY 241 GGCACCTACATTGCCCACTCAATGGCTTAAGCAAGTGTGTGCAGTGCCTCAATGTGAC 300
DB 347 GGCACCTACATTGCCCACTCAATGGCTTAAGCAAGTGTGTGCAGTGCCTCAATGTGAC 406
QY 301 CCAGCCATGGGCTCGCGGAGCGGAGCTGCTCCAGGACAGAGAACCGGTGTGGC 360
DB 407 CCAGCCATGGGCTCGCGGAGCGGAGCTGCTCCAGGACAGAGAACCGGTGTGGC 466
QY 361 TGCAGCCAGGCACTTCTGCATGTCCAGGACGGGACCACTGCGCGGTGCCCGCT 420
DB 467 TGCAGCCAGGCACTTCTGCATGTCCAGGACGGGACCACTGCGCGGTGCCCGCT 526
QY 421 TACGCCACTCCAGCCCGGCGGAGGCTGACAGGAGGACCGAGTCCAGGACACC 480
DB 527 TACGCCACTCCAGCCCGGCGGAGGCTGACAGGAGGACCGAGTCCAGGACACC 586
QY 481 CTGTGTGAGAACTGCCCCCGGGACCTTCTCTCCCAATGGGACCTCGGAGGAATGTGAC 540
DB 587 CTGTGTGAGAACTGCCCCCGGGACCTTCTCTCCCAATGGGACCTCGGAGGAATGTGAC 646
QY 541 CACGAGCAATGGCTTAATCATATGTGTGAAGAAAGCAAGCCAGGGG 591
DB 647 CACGAGCAATGGCTTAATCATATGTGTGAAGAAAGCAAGCCAGGGG 697

RESULT 3

US-09-924-231-6
Sequence 6, Application US/09924231
Patent No. US20020102644A1
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
TITLE OF INVENTION: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/924,231
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 09/333,279
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 4622
TYPE: DNA
ORGANISM: Homo sapiens
US-09-924-231-6

Query Match 93.5%; Score 552.6; DB 9; Length 4622;
Best Local Similarity 98.4%; Pred. No. 3.7e-155;
Matches 558; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
1 ATGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCGAGTGC 60
64 ATGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCGAGTGC 123
61 TTGAGGCTGGTCTGTATCTCACCTTTCTGGAGCCCTCTGCTACGCCCCAGCTCTGCCG 120
124 TTGAGGCTGGTCTGTATCTCACCTTCTGGAGCCCTCTGCTACGCCCCAGCTCTGCCG 183
121 TCTTCAGAGGAGGAGTACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCATCCAGGT 180
184 TCTTCAGAGGAGGAGTACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCATCCAGGT 243
181 TATCTGTGAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTCCCTCCA 240

244 TATCGTGTGAAGGAGCTCGGGAGCTGACGGGCACAGTGTGTGAACCTGCCCTCCA 303
241 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTGTGAGTGCACAAATGTGTGAC 300
304 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTGTGAGTGCACAAATGTGTGAC 363
301 CCAGCCATGGGCTCGGGAGCGGAGCTGCTCCAGGACAGAGAACGGCGTGTGTGGC 360
364 CAGCCATGGGCTCGGGAGCGGAGCTGCTCCAGGACAGAGAACGGCGTGTGTGGC 423
361 TGCAGCCAGGCACTTCTGCACTGCTCCAGGACCGGACCACTCGCGCGTGTGTGGC 420
424 TGCAGCCAGGCACTTCTGCACTGCTCCAGGACCGGACCACTCGCGCGTGTGTGGC 483
421 TACGCACTCCAGCCCGGAGCGGAGCTGCTCCAGGACCGGACCACTCGCGCGTGTGTGGC 480
484 TACGCACTCCAGCCCGGAGCGGAGCTGCTCCAGGACCGGACCACTCGCGCGTGTGTGGC 543
481 CTGTGTGAGAACTGCCCCCGGGAGCTTCTCTCCAAATGGGACCTTGTGAGGAAATGTGAC 540
544 CTGTGTGAGAACTGCCCCCGGGAGCTTCTCTCCAAATGGGACCTTGTGAGGAAATGTGAC 603
541 CACGACCAATGGCTTATCATATG 567
604 CACGACCAATGGCTTATCATATG 630

JULT 4

09-934-289A-43
Sequence 43, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: MB1098-061CIP1(M)
CURRENT APPLICATION NUMBER: US/09/934,289A
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 43
LENGTH: 831
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(831)
-09-934-289A-43

Query Match 93.2%; Score 550.8; DB 9; Length 831;
Best Local Similarity 99.6%; Pred. No. 1e-154;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1 ATGGAGCTCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCAGAACCGAGTC 60
1 ATGGAGCTCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCAGAACCGAGTC 60
61 TTGAGCTGTGTGTATCTACCTTTCTGGGAGCCCTGCTACGCCCTGCGCTGCGG 120
61 TTGAGCTGTGTGTATCTACCTTTCTGGGAGCCCTGCTACGCCCTGCGCTGCGG 120
121 TCCTGCAAGGAGGACGAGTACCGAGTGGGCTCGAGTGTGCTGCCCAAGTGCAGTCCAGGT 180
121 TCCTGCAAGGAGGACGAGTACCGAGTGGGCTCGAGTGTGCTGCCCAAGTGCAGTCCAGGT 180
181 TATCGTGTGAAGGAGGCTCGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 240
181 TATCGTGTGAAGGAGGCTCGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 240

241 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTGTGAGTGCACAAATGTGTGAC 300
241 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTGTGAGTGCACAAATGTGTGAC 300
301 CCAGCCATGGGCTCGGGAGCGGAGCTGCTCCAGGACAGAGAACGGCGTGTGTGGC 360
301 CCAGCCATGGGCTCGGGAGCGGAGCTGCTCCAGGACAGAGAACGGCGTGTGTGGC 360
361 TGCAGCCAGGCACTTCTGCACTGCTCCAGGACCGGACCACTCGCGCGTGTGTGGC 420
361 TGCAGCCAGGCACTTCTGCACTGCTCCAGGACCGGACCACTCGCGCGTGTGTGGC 420
421 TACGCACTCCAGCCCGGAGCGGAGCTGCTCCAGGACCGGACCACTCGCGCGTGTGTGGC 480
421 TACGCACTCCAGCCCGGAGCGGAGCTGCTCCAGGACCGGACCACTCGCGCGTGTGTGGC 480
481 CTGTGTGAGAACTGCCCCCGGGAGCTTCTCTCCAAATGGGACCTTGTGAGGAAATGTGAC 540
481 CTGTGTGAGAACTGCCCCCGGGAGCTTCTCTCCAAATGGGACCTTGTGAGGAAATGTGAC 540
541 CACGACCAATGG 554
541 CACGACCAATGG 554

RESULT 5

US-09-924-231-1
Sequence 1, Application US/09924231
Patent No. US20020102644A1
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/924,231
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 09/333,279
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1724
TYPE: DNA
ORGANISM: Homo sapiens
US-09-924-231-1

Query Match 93.2%; Score 550.8; DB 9; Length 1724;
Best Local Similarity 99.6%; Pred. No. 1e-154;
Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1 ATGGAGCTCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCAGAACCGAGTC 60
294 ATGGAGCTCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCAGAACCGAGTC 353
61 TTGAGCTGTGTGTATCTACCTTTCTGGGAGCCCTGCTACGCCCTGCGCTGCGG 120
354 TTGAGCTGTGTGTATCTACCTTTCTGGGAGCCCTGCTACGCCCTGCGCTGCGG 413
121 TCCTGCAAGGAGGACGAGTACCGAGTGGGCTCGAGTGTGCTGCCCAAGTGCAGTCCAGGT 180
414 TCCTGCAAGGAGGACGAGTACCGAGTGGGCTCGAGTGTGCTGCCCAAGTGCAGTCCAGGT 473
181 TATCGTGTGAAGGAGGCTGCGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 240
474 TATCGTGTGAAGGAGGCTGCGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 533
241 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTGTGAGTGCACAAATGTGTGAC 300
534 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTGTGAGTGCACAAATGTGTGAC 593
301 CCAGCCATGGGCTCGGGAGCGGAGCTGCTCCAGGACAGAGAACGGCGTGTGTGGC 360

b 594 CCAGCCATGGGCTCGCGCGAGCGGAACCTCTCCAGGACAGAGAACGCCGTGTGTGGC 653
y 361 TGCAGCCAGGCGCACTTCTGATCTCCAGACGGGACCACTGCGCGCGGTGCGCGCT 420
b 654 TGCAGCCAGGCGCACTTCTGATCTCCAGACGGGACCACTGCGCGCGGTGCGCGCT 713
y 421 TAGCCACCTCCAGCCCGCGGCGAGAGGTGAGAGAGGAGGACCGAGAGTCAAGACACC 480
b 714 TAGCCACCTCCAGCCCGCGGCGAGAGGTGAGAGAGGAGGACCGAGAGTCAAGACACC 773
y 481 CTGTGTCAAGAACTGCCCCCGGGGACCTTCTCTCCAAATGGGACCTTGGAGGAATGTGAG 540
b 774 CTGTGTCAAGAACTGCCCCCGGGGACCTTCTCTCCAAATGGGACCTTGGAGGAATGTGAG 833
y 541 CACCAGACCAATTG 554
b 834 CACCAGACCAAGTG 847

RESULT 6

S-09-934-289A-14

Sequence 14, Application US/09934289A

Patent No. US20020132297A1

GENERAL INFORMATION:

APPLICANT: Busfield, Samantha J.

TITLE OF INVENTION: NOVEL MOLECULES OF THE

TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: MBIO98-061CPLCN1(M)

CURRENT APPLICATION NUMBER: US/09/934,289A

CURRENT FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: US 09/342,767

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: US 09/146,950

PRIOR FILING DATE: 1998-09-03

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 14

LENGTH: 1724

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (294)...(1142)

S-09-934-289A-14

Query Match 93.2%; Score 550.8; DB 9; Length 1724;

Best Local Similarity 99.6%; Pred. No. 1.1e-154;

Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 1 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCGAGTC 60
b 294 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCGAGTC 353
y 61 TTGAGCTGGTGTATCTACCTTTCTGGAGCCCCCTCTAGCCCCAGCTCTGCCG 120
b 354 TTGAGCTGGTGTATCTACCTTTCTGGAGCCCCCTCTAGCCCCAGCTCTGCCG 413
y 121 TCTTCAAGGAGGACGAGTACCACTGGGCTCCGAGTCTGCCAGTCCAGTCCAGGT 180
b 414 TCTTCAAGGAGGACGAGTACCACTGGGCTCCGAGTCTGCCAGTCCAGTCCAGGT 473
y 181 TATCGTGTGAAGAGGCTCGCGGGAGTGCAGGGACAGTGTGTGAACCTGCCCTCCA 240
b 474 TATCGTGTGAAGAGGCTCGCGGGAGTGCAGGGACAGTGTGTGAACCTGCCCTCCA 533
y 241 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAAGTCCAAATGTGAC 300
b 534 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAAGTCCAAATGTGAC 593
y 301 CCAGCCATGGGCTCGCGCGAGCGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGC 360
b 594 CCAGCCATGGGCTCGCGCGAGCGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGC 653

RESULT 7

US-10-369-300-1

Sequence 1, Application US/10369300

Publication No. US2003021542A1

GENERAL INFORMATION:

APPLICANT: Fraser, Christopher

APPLICANT: Hancock, Wayne

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF

TITLE OF INVENTION: IMMUNE

TITLE OF INVENTION: DISORDERS USING COMBINATION THERAPY

FILE REFERENCE: 7853-255

CURRENT APPLICATION NUMBER: US/10/369,300

CURRENT FILING DATE: 2003-02-19

PRIOR APPLICATION NUMBER: 60/358,463

PRIOR FILING DATE: 2002-02-19

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 1724

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (294)..(1145)

OTHER INFORMATION:

US-10-369-300-1

Query Match 93.2%; Score 550.8; DB 16; Length 1724;

Best Local Similarity 99.6%; Pred. No. 1.1e-154;

Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 1 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCGAGTC 60
b 294 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAGAACCGAGTC 353
y 61 TTGAGCTGGTGTGTATCTACCTTTCTGGAGCCCCCTCTAGCCCCAGCTCTGCCG 120
b 354 TTGAGCTGGTGTGTATCTACCTTTCTGGAGCCCCCTCTAGCCCCAGCTCTGCCG 413
y 121 TCTTCAAGGAGGACGAGTACCACTGGGCTCCGAGTCTGCCAGTCCAGTCCAGGT 180
b 414 TCTTCAAGGAGGACGAGTACCACTGGGCTCCGAGTCTGCCAGTCCAGTCCAGGT 473
y 181 TATCGTGTGAAGAGGCTCGCGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 240
b 474 TATCGTGTGAAGAGGCTCGCGGGAGCTGACGGGACAGTGTGTGAACCTGCCCTCCA 533
y 241 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAAGTCCAAATGTGAC 300
b 534 GGCACCTACATTGCCACCTCAATGGCTTAAGCAAGTGTCTGCAAGTCCAAATGTGAC 593
y 301 CCAGCCATGGGCTCGCGCGAGCGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGC 360
b 594 CCAGCCATGGGCTCGCGCGAGCGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGC 653

361 TGCAGCCAGGCGCACTTCTGTCATCGTCAGGACGGGACCACTGGCGCGGTGCGCGCT 420
421 TAGGCCACTTCAGCCCGCGGCGAGAGGTGCAAGAGGAGGACCGAGAGTCAGGACACC 480
421 TAGGCCACTTCAGCCCGCGGCGAGAGGTGCAAGAGGAGGACCGAGAGTCAGGACACC 480
481 CTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTGAG 540
481 CTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTGAG 540
541 CACCAGACCAATGGGCT 558
541 CACCAGACCAACCGAGCT 558

35ULT 10
3-09-934-289A-1
Sequence 1, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: MB1098-061CPI.CNI (M)
CURRENT APPLICATION NUMBER: US/09/934,289A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1929
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (297)...(875)
3-09-934-289A-1

Query Match 93.1%; Score 550; DB 9; Length 1929;
Best Local Similarity 99.1%; Pred. No. 2e-154;
Matches 553; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
1 ATGAGCCTCTCGAGACTGGGGGCTCTCCCTCGAGATCCACCCCGAGAACCGACGTC 60
297 ATGAGCCTCTCGAGACTGGGGGCTCTCCCTCGAGATCCACCCCGAGAACCGACGTC 356
61 TTGAGGCTGGTCTATCTACCTTTCTGGAGCCCCCTGCTACGCCCGGCTCTGCGG 120
357 TTGAGGCTGGTCTATCTACCTTTCTGGAGCCCCCTGCTACGCCCGGCTCTGCGG 416
121 TCCTGCAAGGAGGACGATACCCAGTGGGCTCCAGAGTCTGCCCAAGTCCAGGT 180
417 TCCTGCAAGGAGGACGATACCCAGTGGGCTCCAGTCTGCCCAAGTCCAGGT 476
181 TATCTGTGAGGAGGCTCTGGGAGCTGACGGGACAGTGTGTGAACCTGCTCCCA 240
477 TATCTGTGAGGAGGCTCTGGGAGCTGACGGGACAGTGTGTGAACCTGCTCCCA 536
241 GGCACCTACATTGCCCACTCAATGGCCCTAAGCAAGTGTCTGCAAGTCCCAATGTGTGAC 300
537 GGCACCTACATTGCCCACTCAATGGCCCTAAGCAAGTGTCTGCAAGTCCCAATGTGTGAC 596
301 CCAGCATGGGCTCTGGGCGAGCGGAACTGTCTCAGGACAGAGAACCGCGTGTGTGGC 360
597 CCAGCATGGGCTCTGGGCGAGCGGAACTGTCTCAGGACAGAGAACCGCGTGTGTGGC 656
361 TCAGCCAGGCGCACTTCTGTCATGTCAGGACGGGACCACTGCGCGGCTGCGCGCT 420
657 TCAGCCAGGCGCACTTCTGTCATGTCAGGACGGGACCACTGCGCGGCTGCGCGCT 716

QY 421 TAGGCCACTTCAGCCCGGCGAGAGGTGCAAGAGGAGGACCGAGAGTCAGGACACC 480
DB 717 TACGCCACTTCAGCCCGGCGGCGAGAGGTGCAAGAGGAGGACCGAGAGTCAGGACACC 776
QY 481 CTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTGAG 540
DB 777 CTGTGTGAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTGAG 836
QY 541 CACCAGACCAATGGGCT 558
DB 837 CACCAGACCAACCGAGCT 854

RESULT 11
US-09-934-289A-31
Sequence 31, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: MB1098-061CPI.CNI (M)
CURRENT APPLICATION NUMBER: US/09/934,289A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 558
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(558)
US-09-934-289A-31

Query Match 92.8%; Score 548.4; DB 9; Length 558;
Best Local Similarity 98.9%; Pred. No. 5e-154;
Matches 552; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
1 ATGAGCCTCTCGAGACTGGGGGCTCTCCCTCGAGATCCACCCCGAGAACCGACGTC 60
1 ATGAGCCTCTCGAGACTGGGGGCTCTCCCTCGAGATCCACCCCGAGAACCGACGTC 60
61 TTGAGGCTGGTCTATCTACCTTTCTGGAGCCCCCTGCTACGCCCGGCTCTGCGG 120
61 TCGAGGCTGGTCTATCTACCTTTCTGGAGCCCCCTGCTACGCCCGGCTCTGCGG 120
121 TCCTGCAAGGAGGACGATACCCAGTGGGCTCCAGAGTCTGCCCAAGTCCAGGT 180
121 TCCTGCAAGGAGGACGATACCCAGTGGGCTCCAGAGTCTGCCCAAGTCCAGGT 180
181 TATCTGTGAGGAGGCTCTGGGAGCTGACGGGACAGTGTGTGAACCTGCTCCCA 240
181 TATCTGTGAGGAGGCTCTGGGAGCTGACGGGACAGTGTGTGAACCTGCTCCCA 240
241 GGCACCTACATTGCCCACTCAATGGCCCTAAGCAAGTGTCTGCAAGTCCCAATGTGTGAC 300
241 GGCACCTACATTGCCCACTCAATGGCCCTAAGCAAGTGTCTGCAAGTCCCAATGTGTGAC 300
301 CCAGCATGGGCTCTGGGCGAGCGGAACTGTCTCAGGACAGAGAACCGCGTGTGTGGC 360
301 CCAGCATGGGCTCTGGGCGAGCGGAACTGTCTCAGGACAGAGAACCGCGTGTGTGGC 360
361 TCAGCCAGGCGCACTTCTGTCATGTCAGGACGGGACCACTGCGCGGCTGCGCGCT 420
361 TCAGCCAGGCGCACTTCTGTCATGTCAGGACGGGACCACTGCGCGGCTGCGCGCT 420

421 TAGCCACCTTCAGCCCGGGCCAGAGGTCAGAGGAGGAGGACCGAGAGTCAGACACC 480
421 TAGCCACCTTCAGCCCGGGCCAGAGGTCAGAGGAGGAGGACCGAGAGTCAGACACC 480
481 CTGTGTCAAGTTCGCCCCCGGGACCTTCTCTCCCAATGGACCTCGAGGAATGTGAG 540
481 CTGTGTCAAGTTCGCCCCCGGGACCTTCTCTCCCAATGGACCTCGAGGAATGTGAG 540
541 CACCAGACCAATGGGCT 558
541 CACCAGACCAAAAGGCT 558

JUL 12

-09-934-289A-29

Sequence 29, Application US/09934289A

Patent No. US20020132297A1

GENERAL INFORMATION:

APPLICANT: Busfield, Samantha J.

TITLE OF INVENTION: NOVEL MOLECULES OF THE

TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: MB1098-061CP1CN1(M)

CURRENT APPLICATION NUMBER: US/09/934,289A

CURRENT FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: US 09/342,767

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: US 09/146,950

PRIOR FILING DATE: 1998-09-03

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 29

LENGTH: 2313

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (85)...(642)

-09-934-289A-29

Query Match

Best Local Similarity 92.8%; Score 548.4; DB 9; Length 2313;

Matches 552; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCAGAACCGAGTC 60
85 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCAGAACCGAGTC 144
61 TTGAGGCTGGTGTATCTACCTTTCTGGGAGCCCTCTGTAGCCGCCAGCTCTGCCG 120
145 TCGAGGCTGGTGTATCTACCTTTCTGGGAGCCCTCTGTAGCCGCCAGCTCTGCCG 204
121 TCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTCTGCCCAAGTGCCAGGT 180
205 TCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTCTGCCCAAGTGCCAGGT 264
181 TATCTGTCAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGACCTGCCCTCCA 240
265 TATCTGTCAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGACCTGCCCTCCA 324
241 GGCACCTACATTGCCACCTCAATGGCCTAAGCAAGTGTCTGCAGTGCCTAAATGTGAC 300
325 GGCACCTACATTGCCACCTCAATGGCCTAAGCAAGTGTCTGCAGTGCCTAAATGTGAC 384
301 CCAGCCATGGGCTCGCGGAGCGGACTGCTCCAGGACAGAGGACCGCGTGTGGC 360
385 CCAGCCATGGGCTCGCGGAGCGGACTGCTCCAGGACAGAGGACCGCGTGTGGC 444
361 TGAGGCCAGGCGACTTCTGTGATCTGTCCAGGACGGGACCACTGCGCGCGTGTGGC 420
445 TGAGGCCAGGCGACTTCTGTGATCTGTCCAGGACGGGACCACTGCGCGCGTGTGGC 504
421 TAGGCCACCTTCAGCCCGGGCCAGAGGTCAGAGGAGGAGGACCGAGAGTCAGACACC 480

Db 505 TAGCCACCTTCAGCCCGGGCCAGAGGTCAGAGGAGGAGGACCGAGAGTCAGACACC 564
QY 481 CTGTGTCAAGTTCGCCCCCGGGACCTTCTCTCCCAATGGACCTCGAGGAATGTGAG 540
Db 565 CTGTGTCAAGTTCGCCCCCGGGACCTTCTCTCCCAATGGACCTCGAGGAATGTGAG 624
QY 541 CACCAGACCAATGGGCT 558
Db 625 CACCAGACCAAAAGGCT 642

RESULT 13

US-10-020-787-1

Sequence 1, Application US/10020787

Publication No. US20020102258A1

GENERAL INFORMATION:

APPLICANT: Harrop, Jeremy A.

APPLICANT: Holmes, Stephen D.

APPLICANT: Reddy, Manjula P.

APPLICANT: Truneh, Alemsseg

TITLE OF INVENTION: Human Tumor Necrosis Factor

TITLE OF INVENTION: Receptor-Like 2 (TR2) Antibodies

FILE REFERENCE: GH50027C1

CURRENT APPLICATION NUMBER: US/10/020,787

CURRENT FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: 09/403,815

PRIOR FILING DATE: 1999-10-26

PRIOR APPLICATION NUMBER: PCT/US98/09744

PRIOR FILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: 60/046,249

PRIOR FILING DATE: 1997-05-12

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1704

TYPE: DNA

ORGANISM: Homo sapien

US-10-020-787-1

Query Match

Best Local Similarity 99.3%; Score 547.6; DB 14; Length 1704;

Matches 550; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCAGAACCGAGTC 60
Db 265 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCTGGAGATCCACCCAGAACCGAGTC 324
QY 61 TTGAGGCTGGTGTATCTACCTTTCTGGGAGCCCTCTGTAGCCGCCAGCTCTGCCG 120
Db 325 TTGAGGCTGGTGTATCTACCTTTCTGGGAGCCCTCTGTAGCCGCCAGCTCTGCCG 384
QY 121 TCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTCTGCCCAAGTGCCAGGT 180
Db 385 TCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTCTGCCCAAGTGCCAGGT 444
QY 181 TATCTGTCAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGACCTGCCCTCCA 240
Db 445 TATCTGTCAAGGAGGCTCGGGGAGCTGACGGGACAGTGTGTGACCTGCCCTCCA 504
QY 241 GGCACCTACATTGCCACCTCAATGGCCTAAGCAAGTGTCTGCAGTGCCTAAATGTGAC 300
Db 505 GGCACCTACATTGCCACCTCAATGGCCTAAGCAAGTGTCTGCAGTGCCTAAATGTGAC 564
QY 301 CCAGCCATGGGCTCGCGGAGCGGACTGCTCCAGGACAGAGGACCGCGTGTGGC 360
Db 565 CCAGCCATGGGCTCGCGGAGCGGACTGCTCCAGGACAGAGGACCGCGTGTGGC 624
QY 361 TGAGGCCAGGCGACTTCTGTGATCTGTCCAGGACGGGACCACTGCGCGCGTGTGGC 420
Db 625 TGAGGCCAGGCGACTTCTGTGATCTGTCCAGGACGGGACCACTGCGCGCGTGTGGC 684
QY 421 TAGGCCACCTTCAGCCCGGGCCAGAGGTCAGAGGAGGAGGACCGAGAGTCAGACACC 480

```

685 TACGCCACCTCCAGCCCGGCGCAGAGGGTGCAGAGGGAGGACCGAGAGTCAGGACACC 744
481 CTGTGTCTAGAACTGCCCGCCCGGAGACCTTCTCTCCCAATGGAGCCCTGGAGGAATGTGAG 540
745 CTGTGTCTAGAACTGCCCGCCCGGAGACCTTCTCTCCCAATGGAGCCCTGGAGGAATGTGAG 804
541 CACCAGACCAATTG 554
805 CACCAGACCAAGTG 818

RESULT 14
3-10-305-720-937
Sequence 937, Application US/10305720
Publication No. US20040010136A1
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
PRIORITY FILING DATE: 2002-11-26
PRIORITY FILING DATE: 09/016,434
PRIORITY FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 937
LENGTH: 976
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040010136A1 778806
FEATURE:
NAME/KEY: unsure
LOCATION: (1) ... (976)
OTHER INFORMATION: a, t, c, g, or other
3-10-305-720-937

Query Match 57.6%; Score 340.2; DB 16; Length 976;
Best Local Similarity 83.2%; Pred. No. 1.1e-91;
Matches 462; Conservative 0; Mismatches 3; Indels 90; Gaps 3;

1 ATGGAGCTCTCGAGAGCTGGGGGCTCTCTCTGGAGATCCACCCCGAGACCGGCTC 60
121 ATGGAGCTCTCGAGAGCTGGGGGCTCTCTCTGGAGATCCACCCCGAGACCGGCTC 180
61 TTGAGGCTGGTGTATCTATCTACCTTTCTGGAGCCCGCTCTACGCCCCAGCTCTGCCG 120
181 TTGAGGCTGGTGTATCTATCTACCTTTCTGGAGCCCGCTCTACGCCCCAGCTCTGCCG 240
121 TCCTCAGAGGAGGACGAGTACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCAGTCCAGGT 180
241 TCCTCAGAGGAGGACGAGTACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCAGTCCAGGT 300
181 TATCGTGTGAAGAGGAGGCTCGCGGAGCTGACGGGACAGTGTGTGAACCTCGCTCCCA 240
301 TA---TGTGAAGAGGAGGCTCGCGGAGCTGACGGGACAGTGTGTGAACCTCGCTCCCA 357
241 GGCACCTACATTGGCCCACTCAATGGCTTAAGCAAGTGTCTGCAGTGCACCAATGTGTGAC 300
358 GGCACCTACATTGGCCCACTCAATGGCTTAAGCAAGTGTCTGCAGTGCACCAATGTGTGAC 417
301 CCAGCATGGGCTCGCGGAGCGGAACTGCTCCAGGACAGAGAACCGCGTGTGTGGC 360
418 ----- 417
361 TGCAGCCAGGACCACTTCTGATCGTCCAGGACGGGACCACTGCGCGCGTCCCGCGCT 420
418 -----CCAGGACGGGACCACTGCGCGCGTCCCGCGCT 451
421 TACGCCACCTCCAGCCCGGCGCAGAGGGTGCAGAGGGAGGACCGAGAGTCAAGACACC 480
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452 TACGCCACCTCCAGCCCGGCGCAGAGGGTGCAGAGGGAGGACCGAGAGTCAAGACACC 511
481 CTGTGTCTAGAACTGCCCGCCCGGAGACCTTCTCTCCCAATGGAGCCCTGGAGGAATGTGCA 539
512 CTGTGTCTAGAACTGCCCGCCCGGAGACCTTCTCTCCCAATGGAGCCCTGGAGGAATGTGCA 571
540 GCACCAGACCAATTG 554
572 GCACCAGACCAAGTG 586

RESULT 15
US-10-369-300-3
Sequence 3, Application US/10369300
Publication No. US20030215442A1
GENERAL INFORMATION:
APPLICANT: Fraser, Christopher
APPLICANT: Hancock, Wayne
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF
TITLE OF INVENTION: IMMUNE
TITLE OF INVENTION: DISORDERS USING COMBINATION THERAPY
FILE REFERENCE: 7853-255
CURRENT APPLICATION NUMBER: US/10/369,300
CURRENT FILING DATE: 2003-02-19
PRIORITY FILING DATE: 2003-02-19
PRIORITY FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1082
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (185) .. (1012)
OTHER INFORMATION:
US-10-369-300-3

Query Match 43.9%; Score 259.6; DB 16; Length 1082;
Best Local Similarity 66.8%; Pred. No. 1.4e-67;
Matches 370; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

1 ATGGAGCTCTCTGGAGACTGGGGCTCTCTCTGGAGATCCACCCCGAGACCGGACGTC 60
185 ATGGAGCTCTCTGGAGATGGGGTGGGACCTCTGGAGCCGCGCTTACAGACACACC 244
61 TTGAGGCTGGTGTATCTACCTTTCTGGAGCCCGCTCTACGCCCCAGCTCTGCCG 120
245 TTGAGGCTGGTGTATCTACCTTTCTGGAGCCCGCTCTACGCCCCAGCTCTGCCG 304
121 TCCTCAGAGGAGGACGAGTACCCAGTGGGCTCCAGTGTCTGCCCAAGTGCAGTCCAGGT 180
305 TCATGCAGACAGGAGGAGTTCCTTTGTGGAGAGCAGTGTCTGCCCAATGTGCACACCAGGT 364
181 TATCGTGTGAAGAGGAGGCTCGCGGAGCTGACGGGACAGTGTGTGAACCTCGCTCCCA 240
365 TACCATGTGAAGCAGGCTCTGAGTGCAGTGCAGTGCAGTGTGTGCCCTGTCTCCCA 424
241 GGCACCTACATTGGCCCACTCAATGGCTTAAGCAAGTGTCTGCAGTGCACCAATGTGTGAC 300
425 CAGACATATACCGCCCAATGCAATGGCTTGCAGTGTGTGCCCTGTGCCGAGTCCGTGAT 484
301 CCAGCATGGGCTCGCGGAGCGGAACTGCTCCAGGACAGAGAACCGCGTGTGTGGC 360
485 CCAGCATGGGCTCGCGGAGCTGCTGCCAGGAGTGTCTCCAGTGCAGGACACTGTGTGACAG 544
361 TGCAGCCAGGACCACTTCTGATCGTCCAGGACGGGACCACTGCGCGCGTCCCGCGCT 420
545 TGCATCCAGGACTCTTCTGTGAGAACCAAGATGGGAGCCACTGTTCACATGCTGTGACAG 604
421 TACGCCACCTCCAGCCCGGCGCAGAGGGTGCAGAGGGAGGACCGAGAGTCAAGACACC 480
605 CACACCACTTGCCTCTCAGGGCAGAGGGTAGAGAGAGGGACTCACGACCGAGGACACT 664
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481 CTGTCAGAACTGCCCCCGGGGACCTTCTCTCCAAATGGGACCCCTGGAGGAATGTCAG 540
665 GTATGTGCTGACTGGCTAACAGGGACCTTCTCACTTGGAGGACTCAGGGAATGCCTG 724
541 CACCAGACCAATTG 554
725 CCTGGACCACTG 738

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Time: 352 secs

GenCore version 5.1.6
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nucleic - nucleic search, using sw model

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(without alignments)
7028.494 Million cell updates/sec

file: US-09-934-289a-19

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Maximum Match 100%

Listing first 45 summaries

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1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estnu.*

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6: em_estpl.*

7: em_estro.*

8: em_hct.*

9: gb_est1.*

10: gb_est2.*

11: gb_hct.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_pq.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

alt	No.	Score	Query Match	Length	DB	ID	Description
1	550.8	93.2	880	12	BI911036	BI911036	603068760
2	550.8	93.2	1012	12	EM912840	EM912840	AGENCOURT
3	550.8	93.2	1200	13	EX436515	EX436515	BC018882
4	550.8	93.2	1612	11	BC018882	Homo sapi	

5	549.2	92.9	867	12	BI908661	BI908661	603066783
6	549.2	92.9	877	12	BI768906	BI768906	603043783
7	549.2	92.9	884	13	BUS28337	BUS28337	AGENCOURT
8	549.2	92.9	928	12	BG761765	BG761765	602717563
9	549.2	92.9	973	12	BG761036	BG761036	602717546
10	549.2	92.9	1040	12	BM928475	BM928475	AGENCOURT
11	549.2	92.9	1046	12	BM919433	BM919433	AGENCOURT
12	549.2	92.9	1057	12	BM546990	BM546990	AGENCOURT
13	549.2	92.9	1068	12	BM920057	BM920057	AGENCOURT
14	549.2	92.9	1106	12	EM808047	EM808047	AGENCOURT
15	546.2	92.4	945	13	BQ646947	BQ646947	AGENCOURT
16	542.8	91.8	863	13	BQ228463	BQ228463	AGENCOURT
17	541.4	91.6	1104	13	EX434044	EX434044	60304044
18	540.8	91.5	895	12	BI761634	BI761634	603046357
19	538.2	91.1	779	12	BI518729	BI518729	603061905
20	538.2	91.1	819	12	BG763109	BG763109	602734992
21	538.2	91.1	856	12	EM014603	EM014603	603640415
22	537.2	90.9	948	13	EX365206	EX365206	60365206
23	536.4	90.8	900	12	BI767552	BI767552	603061455
24	534.2	90.4	681	13	EX103478	EX103478	603043478
25	529.6	89.6	942	13	BO719775	BO719775	AGENCOURT
26	528.8	89.5	1005	12	EM919889	EM919889	AGENCOURT
27	528.4	89.4	1201	9	AL513836	AL513836	603088052
28	526.2	89.0	799	12	BI838914	BI838914	603088052
29	526.2	89.0	825	12	BG766381	BG766381	602739122
30	520.8	88.1	1052	12	EM922691	EM922691	AGENCOURT
31	520.2	88.0	1141	13	EX363980	EX363980	60363980
32	517.6	87.6	940	9	AL553857	AL553857	60363980
33	517.6	87.6	1091	12	EM926437	EM926437	AGENCOURT
34	517.4	87.5	1018	12	EM921865	EM921865	AGENCOURT
35	514.6	87.1	1000	10	BF795808	BF795808	602252337
36	513.6	86.9	763	12	BI839134	BI839134	603090581
37	513	86.8	794	14	CB989754	CB989754	AGENCOURT
38	510.4	86.4	863	12	BG766329	BG766329	602739015
39	509.8	86.3	1071	12	EM915482	EM915482	AGENCOURT
40	507.8	85.9	897	12	BI856292	BI856292	603387535
41	506	85.6	850	12	EM009132	EM009132	603622504
42	485.8	82.2	857	12	BI488633	BI488633	603021165
43	483.2	81.8	816	12	BG765950	BG765950	602738002
44	482.6	81.7	787	12	BI523671	BI523671	603051830
45	482	81.6	754	12	BI752687	BI752687	603021780

ALIGNMENTS

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BI911036
LOCUS 603068760F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5217830 5',
DEFINITION mRNA sequence.
ACCESSION BI911036
VERSION BI911036.1 GI:16174565
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 880)
NIH-MGC http://mgc.ncbi.nlm.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAW11547 row: g column: 15
High quality sequence stop: 834.

481 CTGTGTGAGAACTGCCCCCGGGGAGACTTCTCTCCCAATGGGACCCCTGGAGGAATGTTCAG 540
 561 CTGTGTGAGAACTGCCCCCGGGGAGACTTCTCTCCCAATGGGACCCCTGGAGGAATGTTCAG 620
 541 CACCAGACCAATTG 554
 621 CACCAGACCAAGTG 634

ULT 3
 36515
 'US
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 BX436515 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP002YK21
 5-PRIME mRNA sequence.
 BX436515
 EST.
 BX436515.1 GI:30783475
 Homo sapiens (human)
 Homo sapiens
 Homo sapiens

Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 280.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0CAP002AF11QPI&cluster=280.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0CAP002AF11QPI.
 Location/Qualifiers
 1. .1200
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0CAP002YK21"
 /tissue_type="THYMUS"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

REFERENCE
 AUTHORS
 JOURNAL
 TITLES
 SOURCE

Query Match
 Best Local Similarity 99.6%; Pred. No. 1.5e-113;
 Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAACCGAGTTC 60
 187 ATGGAGCCTCTGGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCGAACCGAGTTC 246

61 TTGAGGCTGTGTGTATCTACCTTCTGGAGGCCCTCTGCTAGCGCCCGAGCTCTGCG 120
 247 TTGAGGCTGTGTGTATCTACCTTCTGGAGGCCCTCTGCTAGCGCCCGAGCTCTGCG 306

121 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTGTCGCCCAAGTGCAGTCCAGGT 180
 307 TCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGTGTCGCCCAAGTGCAGTCCAGGT 366

181 TATCTGTGTGAGAGGACCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTGCCTTCCA 240
 367 TATCTGTGTGAGAGGACCTCGGGGAGCTGACGGGACAGTGTGTGAACCTTGCCTTCCA 426

QY 241 GGCACCTACATTGCCCACTTCAATGGCTTAAGCAAGTGTCTGCAGTGCACCAATGTGTGAC 300
 Db 427 GGCACCTACATTGCCCACTTCAATGGCTTAAGCAAGTGTCTGCAGTGCACCAATGTGTGAC 486
 QY 301 CCAGCCATGGGCTTCGCGCGGAGCGCGAACTGTCTCCAGGACAGAGAACGCCGTGTGTGGC 360
 Db 487 CCAGCCATGGGCTTCGCGCGGAGCGCGAACTGTCTCCAGGACAGAGAACGCCGTGTGTGGC 546
 QY 361 TGCAGCCAGGACCACTTCTGCATGCTCAGACGGGGACCACTGCGCGCGGTGCGCGGCT 420
 Db 547 TGCAGCCAGGACCACTTCTGCATGCTCAGACGGGGACCACTGCGCGCGGTGCGCGGCT 606
 QY 421 TACGCCACCTCCAGCCCGGCGGACAGAGGTGAGAAGGGAGGACCCAGAGTTCAGGACACC 480
 Db 607 TACGCCACCTCCAGCCCGGCGGACAGAGGTGAGAAGGGAGGACCCAGAGTTCAGGACACC 666
 QY 481 CTGTGTGAGAACTGCCCCCGGGGAGACTTCTCTCCCAATGGGACCCCTGGAGGAATGTTCAG 540
 Db 667 CTGTGTGAGAACTGCCCCCGGGGAGACTTCTCTCCCAATGGGACCCCTGGAGGAATGTTCAG 726
 QY 541 CACCAGACCAATTG 554
 Db 727 CACCAGACCAAGTG 740

RESULT 4
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 LOCUS
 DEFINITION
 Homo sapiens tumor necrosis factor receptor superfamily, member 14
 (herpesvirus entry mediator), mRNA (cDNA clone IMAGE:3614371).

ACCESSION
 VERSION
 BC018882.2 GI:33870063
 KEYWORDS
 HTC.
 SOURCE
 Homo sapiens (human)

ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 1612)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE
 JOURNAL
 PUBLISHED
 12477932
 REFERENCE
 2 (bases 1 to 1612)
 Strausberg, R.
 Direct Submission
 Submitted (07-DEC-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK
 COMMENT
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 On Aug 19, 2003 this sequence version replaced gi:17403015.
 Contact: MGC help desk
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCIT/DTF
 cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mc@hgrl.nih.gov

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laris, P., Legaapi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Young, A., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IPAL Plate: 12 Row: n Column: 3
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 10835009
This clone has the following problem: no 5' EST match.

FEATURES

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/tissue type="Skin, melanotic melanoma."
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ACCESSION BI908661
VERSION BI908661.1 GI:16171684
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 867)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L14M11542 Row: e Column: 21
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(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

FEATURES

source
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Location/Qualifiers
/organism="Homo sapiens"
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/clone lib="NIH_MGC_118"
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(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 92.9%; Score 549.2; DB 12; Length 867;
Best Local Similarity 99.5%; Pred. No. 3.1e-113;
Matches 551; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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321 GGCACCTACATGGCCCACTCAATGGCTTAAGCAAGTGTCTGAGTGCACCAATGTGTGAC 380
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 877)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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 stomachs, 62 yo male and 70 yo female. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.4 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 023. Note: this is a NIH_MGC Library."

TUES source

GIN 92.9%; Score 549.2; DB 12; Length 877;

Best Local Similarity 99.5%; Pred. No. 3.1e-113;
 Matches 551; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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 QY 121 TCTTGAAGGAGGAGGATACCCAGTGGGCTCGAGTGTGCCCCAAGTGCAGTCCAGT 180
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LOCUS
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ACCESSION BU528337
 VERSION BU528337.1
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SOURCE
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 884)

TITLE NIH-MGC <http://mgs.nci.nih.gov/>.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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 Location/Qualifiers
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FEATURES
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GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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IGIN

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133  TTGAGGCTGTGTGTATCTCACTTTCTGGAGCCCTCTGTAGCCGCCAGCTCTGCG 192
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ORGANISM Homo sapiens
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REFERENCE

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1 (bases 1 to 928)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 790.
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FEATURES

source

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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_49"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
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Db 434  CCAGCCATGGGCTTGCCTGCGGAGCCGGAACTGCTCCAGGACAGAGAACCCCTGTGTGCG 493
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Db 494  TGCAGCCAGGCGCACCTTCTGATCTGTCAGAGCGGGGACCACTGCGCGCGCGTCCGCGCT 553
Qy 421  TAGGCCACCTTCCAGCCCGGCGCAGAGGCTGTCAGAGGAGGCGCAGGAGTCCAGGACACC 480
Db 554  TAGGCCACCTTCCAGCCCGGCGCAGAGGCTGTCAGAGGAGGCGCAGGAGTCCAGGACACC 613
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81 ATGAGAGCTCTGTGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCHAGAACCGACGTC 140
|||||
61 TTGAGGCTGTGTGATCTACCTTTCTGGAGACCCCTGTACGCCCCAGCTCTGGCG 120
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421 TACGCCACCTTCAGCCCGGCGGAGGCTCAGAGGAGGACCGAGTCCAGGACCACT 480
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481 CTGTGTGAGAACTCCCGCGGAGCACTTCTCTCCCAATGGGACCTCGAGGAATGTGAC 540
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541 CACAGACCAATTTG 554
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621 CACAGACCAATTTG 634
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919433
CUS
FINITION
BM919433 1046 bp mRNA linear EST 12-MAR-2002
AGENCOURT 6715877 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5748693
5', mRNA sequence.
BM919433
BM919433.1 GI:19369812
EST.
ORCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1046)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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/clone_lib="NIH_MGC_120"
/note="Organ: pooled pancreas and spleen; Vector:
pMW-SORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(ScoRV site is destroyed upon cloning). Average insert
size 1.5 Kb, insert size range 1-2.5 Kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
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ORIGIN

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Query Match      92.9%; Score 549.2; DB 12; Length 1046;
Best Local Similarity 99.5%; Pred. No. 3.3e-113;
Matches 551; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAGAGCTCTGTGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCHAGAACCGACGTC 60
DB 81 ATGAGAGCTCTGTGAGACTGGGGGCTCTCTCCCTGGAGATCCACCCCHAGAACCGACGTC 140
QY 61 TTGAGGCTGTGTGATCTACCTTTCTGGAGACCCCTGTACGCCCCAGCTCTGGCG 120
DB 141 TTGAGGCTGTGTGATCTACCTTTCTGGAGACCCCTGTACGCCCCAGCTCTGGCG 200
QY 121 TCTGCAAGGAGGACGAGTACCAAGTGGGCTCCAGTGTGCCCCAAGTGCAGTCCAGT 180
DB 201 TCTGCAAGGAGGACGAGTACCAAGTGGGCTCCAGTGTGCCCCAAGTGCAGTCCAGT 260
QY 181 TATCGTGTGAAGGAGGCTCGGGGAGCTGACGGGCACAGTGTGGAACCTCGCCCTCA 240
DB 261 TATCGTGTGAAGGAGGCTCGGGGAGCTGACGGGCACAGTGTGGAACCTCGCCCTCA 320
QY 241 GGCACCTACATTCGCCACCTCAATGGCCTAAGCAAGTGTGAGTGCACAAATGTGAC 300
DB 321 GGCACCTACATTCGCCACCTCAATGGCCTAAGCAAGTGTGAGTGCACAAATGTGAC 380
QY 301 CCAGCCATGGGCTTGGCGGAGCGGAACTGCTCCAGGACGAGAACCGCTGTGTGGC 360
DB 381 CCAGCCATGGGCTTGGCGGAGCGGAACTGCTCCAGGACGAGAACCGCTGTGTGGC 440
QY 361 TGCAGCCAGGACCACTTCTGATCTGTCAGAGCGGGACCACTTGCGCCCGCTCGCGCT 420
DB 441 TGCAGCCAGGACCACTTCTGATCTGTCAGAGCGGGACCACTTGCGCCCGCTCGCGCT 500
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DB 501 TACGCCACCTTCAGCCCGGCGGAGGCTCAGAGGAGGACCGAGTCCAGGACCACT 560
QY 481 CTGTGTGAGAACTCCCGCGGAGCACTTCTCTCCCAATGGGACCTCGAGGAATGTGAC 540
DB 561 CTGTGTGAGAACTCCCGCGGAGCACTTCTCTCCCAATGGGACCTCGAGGAATGTGAC 620
QY 541 CACAGACCAATTTG 554
DB 621 CACAGACCAATTTG 634
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RESULT 12
BM546990
LOCUS
DEFINITION
AGENCOURT 6491298 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5723783
5', mRNA sequence.
ACCESSION
BM546990
VERSION
BM546990.1 GI:18780404
KEYWORDS
Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1057)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12711 row: p column: 24
High quality sequence start: 16
High quality sequence stop: 689.

TUES

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/clone_lib="NIH_MGC_125"
/notes="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."

3IN

Query Match 92.9%; Score 549.2; DB 12; Length 1057;
est Local Similarity 99.5%; Pred. No. 3.3e-113;
atches 551; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1 ATGAGCCTCTGAGACTGGGGCCCTCTCCCTGGAGATCCACCCGAGACCGACGTC 60
101 ATGAGCCTCTGAGACTGGGGCCCTCTCCCTGGAGATCCACCCGAGACCGACGTC 160
61 TTGAGGCTGGTGTATCTACCTTTCTGGAGCCCTGCTACGCCCGCAGCTCTGCCG 120
161 TTGAGGCTGGTGTATCTACCTTTCTGGAGCCCTGCTACGCCCGCAGCTCTGCCG 220
121 TCCTGCAAGGAGGACGAGTACCCAGTGGGTCCGAGTGTGCCCCCAAGTGCAGTCCAGT 180
221 TCCTGCAAGGAGGACGAGTACCCAGTGGGTCCGAGTGTGCCCCCAAGTGCAGTCCAGT 280
181 TATCGTGTGAGGAGGCTGGGGAGCTGACGGGACAGTGTGAACCTGCCCTCCA 240
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341 GGCACCTACATTGGCCCACTCAATGGCTTAAGCAAGTGTCTGAGTGCACCAATGTGTGAC 400
301 CCAGCCATGGGCTCGGGCGAGCCGAACTGTCTCAGGACAGAGAACCGCGTGTGTCG 360
401 CCAGCCATGGGCTCGGGCGAGCCGAACTGTCTCAGGACAGAGAACCGCGTGTGTCG 460
361 TGCAGCCAGGACCTCTGATCTGTCAGGACGGGACCACTGCGCGCGGTGTCGCGCT 420
461 TGCAGCCAGGACCTCTGATCTGTCAGGACGGGACCACTGCGCGCGGTGTCGCGCT 520
421 TACGCCACCTCCAGCCCGGCGCAGAGGTCAGAGGAGGACCGAGAGTTCAGGACAC 480
521 TACGCCACCTCCAGCCCGGCGCAGAGGTCAGAGGAGGACCGAGAGTTCAGGACAC 580

QY 481 CTGTGTGAGAACTCCCGCGGAGACTTCTTCCAAATGGGACCTGGAGAAATCTCAG 540
Db 581 CTGTGTGAGAACTCCCGCGGAGACTTCTTCCAAATGGGACCTGGAGAAATCTCAG 640
QY 541 CACCAGACCAATTG 554
Db 641 CACCAGACCAATTG 654

RESULT 13
BM920057 1068 bp mRNA linear EST 12-MAR-2002
LOCUS AGENCOURT_6706583 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5749919
DEFINITION 5', mRNA sequence.

ACCESSION BM920057
VERSION BM920057.1 GI:19370436
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1068)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12780 row: a column: 24
High quality sequence stop: 674.

FEATURES
Location/Qualifiers
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/notes="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 92.9%; Score 549.2; DB 12; Length 1068;
Best Local Similarity 99.5%; Pred. No. 3.3e-113;
Matches 551; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAGGCTCTGAGACTGGGGCCCTCTCCCTGGAGATCCACCCGAGACCGACGTC 60
Db 97 ATGAGGCTCTGAGACTGGGGCCCTCTCCCTGGAGATCCACCCGAGACCGACGTC 156
QY 61 TTGAGGCTGGTGTATCTCACTTTCTGGAGAGCCCTCTGTCACGCCCGCAGCTCTGCCG 120
Db 157 TTGAGGCTGGTGTATCTCACTTTCTGGAGAGCCCTCTGTCACGCCCGCAGCTCTGCCG 216
QY 121 TCCTGCAAGGAGGACGAGTACCCAGTGGGTCCGAGTGTGCCCCCAAGTGCAGTCCAGT 180
Db 217 TCCTGCAAGGAGGACGAGTACCCAGTGGGTCCGAGTGTGCCCCCAAGTGCAGTCCAGT 276
QY 181 TATCGTGTGAGGAGGCTCGCGGGAGCTGACGGGACAGTGTGTGAACCCCTGCCCTCCA 240

277 TATCGTGTGAAGAGGCTCGGGGAGCTGACGGCACAGTGTGTGAACCTCGCTCCCA 336
241 GGCACCTTACATTCACCTCAATAGCCCTTAAGCAAGTGTCTGCAAGTGCCTCAATGTGTGAC 300
337 GGCACCTTACATTCACCTCAATAGCCCTTAAGCAAGTGTCTGCAAGTGCCTCAATGTGTGAC 396
301 CAGCCATGAGGCTCGGGGAGGCTGAGGAGGCTGCTCAGGACAGAGAGGCTGTGTGAC 360
397 CAGCCATGAGGCTCGGGGAGGCTGAGGAGGCTGCTCAGGACAGAGAGGCTGTGTGAC 456
361 TGCAGCCATGAGGCTCGGGGAGGCTGAGGAGGCTGCTCAGGACAGAGAGGCTGTGTGAC 420
457 TGCAGCCATGAGGCTCGGGGAGGCTGAGGAGGCTGCTCAGGACAGAGAGGCTGTGTGAC 516
421 TGCAGCCATGAGGCTCGGGGAGGCTGAGGAGGCTGCTCAGGACAGAGAGGCTGTGTGAC 480
517 TGCAGCCATGAGGCTCGGGGAGGCTGAGGAGGCTGCTCAGGACAGAGAGGCTGTGTGAC 576
481 CTGTGTGAGGCTCGGGGAGGCTGAGGAGGCTGCTCAGGACAGAGAGGCTGTGTGAC 540
577 CTGTGTGAGGCTCGGGGAGGCTGAGGAGGCTGCTCAGGACAGAGAGGCTGTGTGAC 636
541 CACGACCAATTTG 554
637 CACGACCAATTTG 650

RESULT 14
4806047
LOCUS
DEFINITION
BMS06047
EST.
SYNOPSIS
SOURCE
ORGANISM

BMS06047 1106 bp mRNA linear EST 05-MAR-2002
AGENCOURT 6513372 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5731803
5', mRNA sequence.
BMS06047
EST.
SYNOPSIS
SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1106)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

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Location/Qualifiers
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/note="Organ: Brain; Vector: pCMV-Sport6; Site: 1: EcorV
(destroyed); Site: 2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcorV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

ORIGIN
Query Match 92.9%; Score 549.2; DB 12; Length 1106;
Best Local Similarity 99.5%; Pred. No. 3.3e-113;
Matches 551; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 61 TTGAGGCTGTGTATCTACCTTTCTGGGAGGCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 140 TTGAGGCTGTGTATCTACCTTTCTGGGAGGCTCTCTCTCTCTCTCTCTCTCTCT 199
QY 121 TCTGCAAGGAGGAGGAGTACCCAGTGGGCTCCGAGTGTCTGCCCAAGTGCAGTCCAGT 180
DB 200 TCTGCAAGGAGGAGGAGTACCCAGTGGGCTCCGAGTGTCTGCCCAAGTGCAGTCCAGT 259
QY 181 TATCGTGTGAAGGAGGCTCTCGGGGAGCTGACGGGACAGTGTGTGAACCTCTGCCCTCCA 240
DB 260 TATCGTGTGAAGGAGGCTCTCGGGGAGCTGACGGGACAGTGTGTGAACCTCTGCCCTCCA 319
QY 241 GGCACCTTACATTCGCCACCTCAATGGCTTAAGCAAGTGTCTGCAAGTGTGTGAC 300
DB 320 GGCACCTTACATTCGCCACCTCAATGGCTTAAGCAAGTGTCTGCAAGTGTGTGAC 379
QY 301 CCAGCCATGAGGCTCTCGGGGAGCTGACGGGACAGTGTGTGAACCTCTGCCCTCCA 360
DB 380 CCAGCCATGAGGCTCTCGGGGAGCTGACGGGACAGTGTGTGAACCTCTGCCCTCCA 439
QY 361 TGCAGCCATGAGGCTCTCGGGGAGCTGACGGGACAGTGTGTGAACCTCTGCCCTCCA 420
DB 440 TGCAGCCATGAGGCTCTCGGGGAGCTGACGGGACAGTGTGTGAACCTCTGCCCTCCA 499
QY 421 TACGCCATCTCCAGCCCGGCTGCAAGGAGGCTGCAAGGAGGCTGCAAGGAGGCTGCAAGGAGGCT 480
DB 500 TACGCCATCTCCAGCCCGGCTGCAAGGAGGCTGCAAGGAGGCTGCAAGGAGGCTGCAAGGAGGCT 559
QY 481 CTGTGTGAGGCTCTCGGGGAGCTGACGGGACAGTGTGTGAACCTCTGCCCTCCA 540
DB 560 CTGTGTGAGGCTCTCGGGGAGCTGACGGGACAGTGTGTGAACCTCTGCCCTCCA 619
QY 541 CACGACCAATTTG 554
DB 620 CACGACCAATTTG 633

RESULT 15
BQ646947
LOCUS
DEFINITION
BQ646947
EST.
SYNOPSIS
SOURCE
ORGANISM

BQ646947 945 bp mRNA linear EST 15-JUL-2002
AGENCOURT 8302463 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6271311
5', mRNA sequence.
BQ646947
EST.
SYNOPSIS
SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 945)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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/note="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

IGIN

Query Match 92.4%; Score 546.2; DB 13; Length 945;
Best Local Similarity 99.5%; Pred. No. 1.5e-112;
Matches 548; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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|||
64 AGGCTGGTCTGTACTCTACCTTCTGGAGCCCTCTAGCGCCCGAGCTCTCGCGTCC 123
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81 AGGCTGGTCTGTACTCTACCTTCTGGAGCCCTCTAGCGCCCGAGCTCTCGCGTCC 140
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124 TGCAGGAGGAGGAGTACCAGTGGGCTCCGAGTGTCTGCCCAAGTGCAGTCCAGGTTAT 183
|||
141 TGCAGGAGGAGGAGTACCAGTGGGCTCCGAGTGTCTGCCCAAGTGCAGTCCAGGTTAT 200
|||
184 CGTGTGAAGAGGCTTGGGGAGCTGACGGGACAGTGTGTGAACCTTGCCTCCAGGC 243
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201 CGTGTGAAGAGGCTTGGGGAGCTGACGGGACAGTGTGTGAACCTTGCCTCCAGGC 260
|||
244 ACCTACATGGCCCACTCAATGGCTAAGCAAGTGTCTGCAGTGCACAAATGTGTGACCCA 303
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261 ACCTACATGGCCCACTCAATGGCTAAGCAAGTGTCTGCAGTGCACAAATGTGTGACCCA 320
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321 GCCATGGGCTTGGCGGAGCGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGCTGC 380
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364 AGCCAGGCGCACTTCTGCATGCTCCAGAGCGGGACACTGCGCGCGTGCCTGCTTAC 423
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381 AGCCAGGCGCACTTCTGCATGCTCCAGAGCGGGACACTGCGCGCGTGCCTGCTTAC 440
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424 GCCACCTCCAGCCCGGCGCAGAGGTGAGAGGAGGACCCGAGAGTCAAGACACCCCTG 483
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